TABEL 1

M

	00-1	hRSV	bRSV	PMV	APV-A	APV-C	APV-B
00-1	1,00	0,37	0,37	0,37	0,77	0,87	0,75
hRSV	---	1,00	0,91	0,41	0,37	0,37	0,37
bRSV	---	---	1,00	0,42	0,35	0,36	0,35
PMV	---	---	---	1,00	0,37	0,38	0,38
APV-A	---	---	---	---	1,00	0,78	0,89
APV-C	---	---	---	---	---	1,00	0,77
APV-B	---	---	---	---	---	---	1,00

N

	00-1	hRSV	bRSV	PVM	APV-A	APV-C	APV-B
00-1	1,00	0,20	0,22	0,21	0,40	0,52	0,40
hRSV	---	1,00	0,59	0,30	0,18	0,21	0,18
bRSV	---	---	1,00	0,31	0,21	0,23	0,21
PVM	---	---	---	1,00	0,21	0,23	0,21
APVA	---	---	---	---	1,00	0,42	1,00
APVC	---	---	---	---	---	1,00	0,42
APVB	---	---	---	---	---	---	1,00

F

	00-1	hRSV	bRSV	PVM	APV-A	APV-C	APV-B
00-1	1,00	0,32	0,33	0,37	0,67	0,80	0,66
hRSV	---	1,00	0,82	0,40	0,35	0,35	0,35
bRSV	---	---	1,00	0,41	0,34	0,36	0,34
PVM	---	---	---	1,00	0,38	0,38	0,39
APV-A	---	---	---	---	1,00	0,72	0,84
APV-C	---	---	---	---	---	1,00	0,72
APV-B	---	---	---	---	---	---	1,00

P

	00-1	hRSV	bRSV	PMV	APV-A	APV-C
00-1	1,00	0,25	0,26	0,27	0,55	0,67
hRSV	---	1,00	0,81	0,30	0,28	0,26
bRSV	---	---	1,00	0,29	0,28	0,26
PMV	---	---	---	1,00	0,23	0,27
APV-A	---	---	---	---	1,00	0,52
APV-C	---	---	---	---	---	1,00

L8

	00-1	hRSV	bRSV	APV-A
00-1	1,00	0,36	0,35	0,56
hRSV	---	1,00	0,79	0,36
bRSV	---	---	1,00	0,35
APV-A	---	---	---	1,00

L9/10

	00-1	hRSV	bRSV	APV-A
00-1	1,00	0,30	0,30	0,53
hRSV	---	1,00	0,83	0,34
bRSV	---	---	1,00	0,32
APV-A	---	---	---	1,00

Fig. 1a

Table 2

Seroprevalence of hMPV in humans categorised by age group using immunofluorescence and virus neutralisation assays

	Immunofluorescence assays		Virus neutralisation assays		
Age (Years)	N tested	N positive	N tested	N positive	Titre range
< 1	20	5	12	3	16-32
1-2	20	11	13	4	16-32
2-5	20	14	8	3	16-512
5-10	20	20	4	4	32-256
10-20	20	20	4	3	32-128
> 20	20	20	4	3	32-128
8-99[1]	72	72	11	11	16-128

[1]Sero-archeological analysis using sera collected in 1958

Fig. 1b

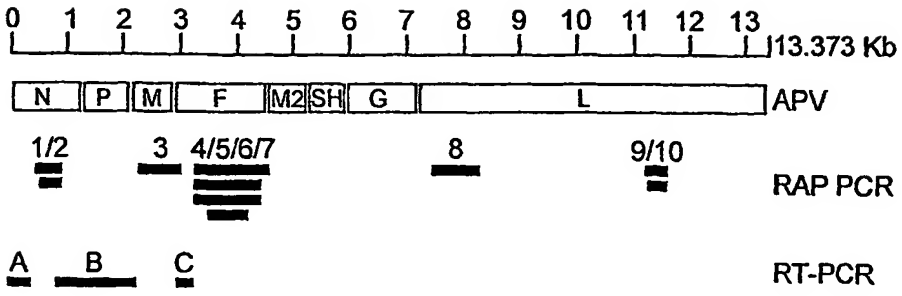

0 1 2 3 4 5 6 7 8 9 10 11 12 13
13.373 Kb
N P M F M2 SH G L
APV
1/2 3 4/5/6/7 8 9/10
RAP PCR
A B C
RT-PCR

Fig. 2

Fig. 3

Nucleo protein

```
00-1 NP MSLQGIHLSDLSYKHAILKESQYTIKRDVGTTTAVTPSSLQQEITLLCGEILYAKHADYKYAAEIGIQYISTALGSERVQQILRNSGSEVQVVLTRTYSL 10
APV A   ...ES.R....E......ED.....R....A...I...E..PQVST...MV.F...T..EP...V.M........AD.T....K.......G.H.KIVT. 10
APV B   ......Q..............................R.VS...........T..SH...V.M..V..T..A..T....K.......A...K.... 10
APV C   ......Q..............................R.VS...........T..SH...V.M..V..T..A..T....K.......A...K.... 10
bRSV    .A.SKVK.N.TFN.DQL.ST.K...Q.ST.DNIDIPNYDV.KHLNK...ML.ITED.NH.FTGL..ML.AMSR..R.DTLK..KDA.YQ.RANGVDVITH 10
hRSV    .A.SKVK.N.TLN.DQL.SS.K...Q.ST.DNIDTPNYDV.KHLNK...ML.ITED.NH.FTGL..ML.AMSR..R.DTIK..KDA.YH.KANGVDITTY 10
PVM     ...DRLK.N.V.N.DSL.SNCK.SVT.ST.DV.S.SGHAM.KALARTL.MF.LTAFNRCEEV....L..AMSL..RDDSIK...EA.YN.KC.D.QLKDF 10

00-1 NP GKIKNNKGEDLQMLDIHGVEKSWVEEIDKEARKTMATLLKESSGNIPQNQRPSAPDTPIILLCVGALIFTKLASTIEVGLETTVRRANRVLSDALKRYPR 20
APV A   SAEGSVRKREV--.N..D.GVG.ADDVERTT.EA.GAMVR.KV-QLTK..K...L.A.V....I...........V......AI...S......IS.... 19
APV B   ..G..S...E..........R..I..V.........SAT.DN..P........S..A......I..................A........N.....F.. 20
APV C   ..G..S...E..........R..I..V.........SAT.DN..P........S..A......I..................A........N.....F.. 20
bRSV    RQDV.G.EMKFEV.TLVSLTSEVQGN.EI.S..SYKKM...M-.EVAPEY.HDS..CGM.V...A..VI....AGDRS..TAVI....N..RNEM...KG 19
hRSV    RQDI.G.EMKFEV.TLSSLTSEIQVN.EI.S..SYKKM...M-.EVAPEY.HDS..CGM.I..IA..VI....AGDRS..TAVI....N..KNEI...KG 19
PVM     TIKLQG.EYKI.V...V.IDAANLADLEIQ..GVV.KE..TG-ARL.D.R.HD...CGV.V..IA..VVS...AGDRG..DAVE...LN..KAEKA...N 19

00-1 NP MDIPKIARSFYDLFEQKVYHRSLFIEYGKALGSSSTGSKAESLFVNIFMQAYGAGQTMLRWGVIARSSNNIMLGHVSVQAELKQVTEVYDLVREMGPESG 30
APV A   ....R..K..FE...K...Y.N...........T....RM.......................................R..S.......K...... 29
APV B   I..................Y.................................................................................... 30
APV C   I..................Y.................................................................................... 30
bRSV    LIPKD..N...EV..KYPHYIDV.VHF.I.QS.TRG..RV.GI.AGL..N......V......L.K.VK......A.....ME..V...EYAQKL.G.A. 29
hRSV    LIPKD..N...EV..KHPHLIDV.VHF.I.QS.TRG..RV.GI.AGL..N...S..V......L.K.VK......A.....ME..V...EYAQKL.G.A. 29
PVM     .EVKQ..E.......R.P.YIDV..TF.L.QS.VRG...V.G..SGL..N......V.....LL.K.VK......A.....ME..V...EYAQKQ.G.A. 29

00-1 NP LLHLRQSPKAGLLSLANCPNFASVVLGNASGLGIIGMYRGRVPNTELFSAAESYAKSLKESNKINFSSLGLTDEEKEAAEHFLNVSDDSQNDYE       39
APV A   ................T..............A........K..A..L...A......RT.R.N....LAA.....D.R...TSY.GGD.ERSSKF.       39
APV B   ......N...........................L.............A......R.................E.......N...INEEG.....       39
APV C   ......N...........................L.............A......R.................E.......N...INEEG.....       39
bRSV    FY.ILNN...S....TQF...S.......A....M.E...TPR.QD.YD..KA..EQ...NGV..Y.V.D..T..L..IKNQ..PK.N--DVEL       39
hRSV    FY.ILNN...S....TQF...S.......A....M.E...TPR.QD.YD..KA..EQ...NGV..Y.V.D..A..L..IKNQ..PKE.--DVEL       39
PVM     FY.I.NN...S....T.....T.......A......S.K.APR.R...D..KD..ER..DN.V..Y.A.N..A..R.LISQQ..IV..TPD.DI       39
```

Phospho protein

```
00-1 P MS-PPEGKDILFMGNEAAKLAEAF--------QKSLRKPGHKRSQSIIGEKVNTVSETLELPTISRPAKPTIPSEPKLAWTDKGGATKTEIKQAIKVMDP 91
APV-A  ..-........M..S....M.D.Y--------.R...NTSAG-GR..S..PI..IA.KVP..PLCN.TT.-------------..SCI.PNKAPVP..K-- 76
APV-C  ..-........L.......A....--------.R..K.I..R.T...V.D.II.....V.K....KST.V.T.P.R.N..GE.PDT.RSQTEE.RNEAT. 91
bRSV   .-------------...........--------........................................................................ 80
hRSV   .EK.APE----.H.ED.NNK.TK.LES---------------------------------IKGKF-------------------------ASSKDPKK.DS.ISVNS 45
PVM    .EK.APE----.V.ED.N.K..E.LKHRSFPSE.P.AGIPNTATHVTKYNMPPILRSSFK..SPRVA.NL.E..A.-----PTTPPP.PPQN.EEQPKESD 92

00-1 P IEEEESTEKKVLPSSDGKTPAEKKLKPSTNT------KKKVSFTPNEP---GKYTKLEKDALDLLSDNEEEDAE-SSILTFEE---RDTSSLSIEARLESIE 18
APV-A  ---.I..IYP.LPTAPVATDTYTSTSTE.AKK------S...K.DNPKV---.......EEG.E....P..DND.K........---K..A.T.......A.. 16
APV-C  EDASRLY.EVEA.T.........GKETPEKP------....T.KND.S---.R.....ME..E......DD...-..V.....---K...A..L.......D 18
bRSV   ...............................------...........---.........................-........---................ 16
hRSV   .DI.VTK.SPITSGTNIIN.TSEADSTPETKANYPR.PL...KEDLTPSDNPFS..Y.ETIETF----DNN---.EE.SYSY..INDQ.-NDN.T...DR.D 13
PVM    VDI.TMHVC..PDNPEHSKKPCCSDDTD.KKT---R.PM.T.VEP.EKFV.LGAS.YRETMQTF----AADGYDEE.N.S...TNQEPG.S.V.Q..DR.. 18

00-1 P EKLSMILGLLRTLNIATAGPTAARDGIRDAMIGVREELIADIIKEA---KGKAAEM----MEEEMXQRSKIGNGSVKLTEKAKELNKIVEDESTSGESEEE 27
APV-A  ........M.K.......................M.....NS.MT..---.D.I...----.K..DT..A...D...............L..Q.S.....S. 25
APV-C  ...............V.................V.L............---.......----.K..AK.K........G......................... 27
bRSV   ................................................---.......----.....X.................................. 26
hRSV   ....E...M.H..VV.S....S.........V.L...M.EK.RA..LMTNDRLEA.ARLRN..SEKMA.DTSDE.P.NPTS.K.SDLL..N---------- 23
PVM    ....Y.I...N.IMV......T...E....L..T.....EM.KSDILTVNDRIVA.EKLRD..CSRADTDDGSACY..DR.RI.D...SSNA--------- 27

00-1 P EEPKDTQDNSQEDDIY----QLIM.                                                                            29
APV-A  ..SGESESDEE.S...NLDL-.L                                                                              28
APV-C  ..EE.EEESNPD..L.SLTM-.LIKN                                                                           29
bRSV   ................----.....                                                                            28
hRSV   -----.SDNDLSL.--------DF.                                                                            24
PVM    ---EEAKEDLDV...MGINF-.LI                                                                             29
```

Matrix protein

Fig. 3, contd.

```
00-1 matrix MESYLVDTYQGIPYTAAVQVDLIEKDLLPASLTIWFPLFQANTPPAVLLDQLKTLTITTLYAASQNGPILKVNASAQGAAMFVLPKKFEVNATVAXDEYS 10
APV-B       ....II.....V..........V...NN..K..V......SS..AP.........S...Q.TV.PE..V.Q...T......SA.....S.S.AA.L.... 10
APV-A       ....II.....V..............SN..T..V......SS..AP.........S...Q.T..PE..V.Q...A......SA.....A.S.A..L.... 10
APV-C       ..........V.......T..V...Q...R..V.V....T....T...E..........T.....................SA...S.D.S.S..L.D.. 10
bRSV        ..T.VNKLHE.ST......YNV....DD.......V.M..SSISADL.IKE.INVN.LVRQISTLK..S..IMINSRS.VLAQM.S..TIS.N.SL..R. 10
hRSV        ..T.VNKLHE.ST......YNVL...DD.......V.M..SSV.ADL.IKE.ASIN.LVKQISTPK..S.R.TINSRS.VLAQM.SN.IIS.N.SL..R. 10
PVM         ..A...EM.H.V.......LN.V..HSANI...V.I.M..TSL.KNSVM.L.HDV.VICTQISTVH..MI..DL.SSN.GLATM.RQ.LI..II.L.DWG 10

00-1 matrix KLEFDKLTVCEVKTVYLTTMKPYGMVSKFVSSAKSVGKKTHDLIALCDFMDLEKNTPVTIPAFIKSVSIKESESATVEAAISSERDQALTQAKIAPYAGL 20
APV-B       ..D.GV....D.RA.....L........I.TNMNT..R...........I.M.RGI......Y..A....D...........G.....I...R....... 20
APV-A       R...GT....D.RSI....L........IMTDVR...R...........I.I..GV.I....Y..A....D...........G.....I...R....... 20
APV-C       ..........L.A..............N...A.............L....GV......Y..................G.....I...R....... 20
bRSV        ..AY.IT.P..I.ACS..CL.VKN.LTTVKDLTMKTFNP..EI....E.ENIMTSKR.V..T.LR.INV.AKDLDSL.NIATT.FKN.I.N...I..... 20
hRSV        ..AY.VT.P..I.ACS..CL.VKS.LTTVKDLTMKTFNP..EI....E.ENIMTSKR.I..TYLRPI.V.NKDLNSL.NIATT.FKN.I.N...I..... 20
PVM         NMDYEVPVAFDK.SFCV.IL..KN.LYTVP.ITPTN-RP..E...V.S.HNRVTLKSFN..V..RALY.RQQGLDS..Q....DV.H.I.T.RV...... 19

00-1 matrix IMIMTMNNPKGIFKKLGAGTQVIVELGAYVQAESISKICKTWSHQGTRYVLKSR.                                              25
APV-B       .LL.A........R.............P......LG......N..R...———I———L—K———SR                                  25
APV-A       .L.................M.......P......LG......N..R.....R...-.GYPK-A.-IC.C-YSQ.K                        27
APV-C       ..................V.................R..RN...........————————————R                                    25
bRSV        VLVI.VTDN..A..YIKPQS.F..D....LEK...YYVTTN.K.TA.KFSI.P————————————IED.                               25
hRSV        VLVI.VTDN..A..YIKPQS.F..D....LEK...YYVTTN.K.TA..FSI.P————————————LED.                               25
PVM         TLVINITST..A..L.K..S.IIA...P.LTQV.LHDVIMN.K.T..S.I...SS————————————TSG.                              25
```

Fusion protein

```
00-1 F MSW———KVVIXFSLLI———————TPXHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEVGDVENLTCADGPS———LIKTELDLTKSALRELRTVSADQ 88
APV-A  .DV———RICLLLF.IS———————N.SSCIQ.T.N.....V.R..K...........N..I.N...I..N....———..D...V...N.....K..... 88
APV-B  .YL———.LLLIIY.VV———————GASGKIQ.T.S.....V.R..K...........N..I.N...I..N....———..S...S..QN..Q........ 88
APV-C  ...———...LLLV..A———————..TG..E.....Y..V.R.....................T....———..R...E...N..E..K..... 88
bRSV   .ATTAMRMI.SIIFISTYVTHI.LCQNIT.EFYQST..AVSR....A.....S.V.I.LSKIQKNV.KSTD.KVK...Q..ERYNN.VV..QSLMQNE 10
hRSV   .ELLIHRLSAI.LT.AINALYL.SSQNIT.EFYQST..AVSR..f.A.....S.I.I.LSNIKETK.NGTDTKVK...Q...KY.N.VT..QLLMQNT 10
PVM    .———IPGR.FLV..VIFNTKPIHPNT.T.K.Y.ST..VE.A..K.A.....HMT.MSIKLSQINIES.KSSN.———.LAH..AIYS..VD....L.SNA 93

00-1 F LAREEQ———————————————————IENPRQSRFVLGAIALGVATAAAVTAGVAIAKTIRLESEVTAIKNALKKTNEAVSTLGNGVRVLATAVRELK 16
APV-A  V.K.SR———————————————————LSS..RR.....................L.....G..K.....RN.....................ND.. 16
APV-B  ITK.NR———————————————————.LSH.KK.....T.....L.....G..K...L..RS.....I.....ND.. 16
APV-C  ..K.AR———————————————————.MS..KA.....G..A...G..R.....ND.. 16
bRSV   P.SFSRAKRGIPELIHYTRNSTKKFYGLMGKK.KR..L—GFL..IG—S..AS...VS.VLH..G..NK.....LS..K..VS.S...S..TSK.LD.. 19
hRSV   P.ANNRARREAPQYMNYTINTTKNLNVS.SKK.KR..L—GFL...G—S.IAS.I.VS.VLH..G..NK.....LS..K..VS.S...S..TSK.LD.. 19
PVM    ————————————————————————LKSK.KK..L—GLI..LG—.....L...VQ....IAL.RD.VRN.....VS.T..MS...KV.DD.. 16

00-1 F DFVSKNLTRAINKNKCDIADLKMAVSFSQFNRRFLNVVRQFSDNAGITPAISLDLMTDAELARAVSNMPTSAGQIKLMLENRAMVRRKGFGFLIGVYGSS 26
APV-A  E.I..K..P...Q...N...I...I..G.N.....S....S.V.....D..V..INR....S...S...N.....I.....DGT 26
APV-B  E.I..K..P...Q...N...IR..I..G.N.....S....S.V.....VK.INR....S...S...N.....I.....GT 26
APV-C  ..I..K..P...R.....S.....G.Y.....V.....S...N.....I.....  26
bRSV   NYID.E.LPQV.NHD.R.SNIETVIE.Q.K.N.L.EIA.E..V.....TPL.TYML.NS..LSLIND..ITND.K...SS.VQI..QQSYSIMSV.KEEV 29
hRSV   NYINNQ.LPIV.QQS.R.SNIETVIE.Q.K.S.L.EIN.E..V...V.TPL.TYML.NS..LSLIND..ITND.K...SS.VQI..QQSYSIMSIIKEEV 29
PVM    N.I..E.LPK..RVS..VH.ITAVIR.Q.L.K.L.E.S.E..S...L.HTV.SFML..R..TSI.GG.AV....KEI..SSK.IM..N.LAI.SS.NADT 26

00-1 F VIKMVQLPIFGVIDTPCWIVKAAPSC—SGKKGNYACLLREDQGWYCQNAGSTVYYPNEKDCETRGDHVFCDTAAGINVAEQSKECNINISTTNYPCKVS 36
APV-A  .VY.....E....R.V...L.—RKE.....I.....T.....A....KD...V.D.Y.....LEVEQ..Y....SK..... 36
APV-B  .VY.....E....R.V...L.—RHERES.....T.....A....D...V.D.Y.....SEVEQ..H....ST..... 36
APV-C  .VYI.....K.....L.—...D.....E...V.S.....KE.E...R.....K..... 36
bRSV   IAYV.....Y.....KLHTS.L.TTDN.E.SNI..T.T.R....D....VSFF.QTET.KVQSNR.....MNSLTLPTDVNL..TD.FN.K.D..IM 39
hRSV   LAYV.....Y.....KLHTS.L.TTNI.E.SNI..T.T.R....D....VSFF.QADT.KVQSNR.....MNSLTLPSEVSL..TD.FNSK.D..IM 39
PVM    LVYVI...L...M..D..VIRSSID.—HNIADK....A.A.N....H....LS.F.SPT...IHNGYA....LKSLT.PVT.R...S.MY....D..I. 35

00-1 F TGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIIKQLNKGCSYITNQDADTVTIDNTVYQLSKVEGEQHVIKGRPVSSSFDPVKFPEDQFNVALDQVF 46
APV-A  .....V.....T...G..S..ES.....K.....G...TH.P.NE...I.....V...RT...A..VNN.N.IL..... 46
APV-B  .....V.....T...G..S..E.....K.....TH.P.NE...I.....I.....V...RT...A..VNN.N.LL..... 46
APV-C  .....D.M.....K....RP.G.....S.....T...K....N...IE.....I..... 46
bRSV   .SKTD..SSVITSI..I.S..GKTK.TASNKNR....TFSN..D.VS.KGV...SVG..L.YVN.L..KALY...E.IINYY..LV..S.E.DASIA..N 49
hRSV   .SKTD..SSVITS...I.S..GKTK.TASNKNR....TFSN..D.VS.KGV...SVG..L.YVN.L..KNLYV..E.IINYY..LV..S.E.DASIS..N 49
PVM    .SKTYV.TAV.TIM.C..S..GHN..TVIN.DK...RT.PD..H..S.KGV.R.QVG....Y...EV.KSI.VR.E.LVLKY..LS..D.K.D..IRD.E 45

00-1 F ESIENSQALVDQSNRILS———SAEKGNTGFII—VIILIAVLGSTMILVSVFIIIKKTKRPTGAP-PELSGVTNNGFIPH-N.                    54
APV-A  ...DR..D.I.K..DL.G———ADA.SKA.IA.—A.VVLVI..IFFL.AVIYYCSRVR.TKPKHDY.ATT.HSSMAYV————————S              53
APV-B  ..VDK.KD.I.K..DL.D———IEV.S.I.AAL—A.TILV..SMLI.VGIAYYVV..R.AK.SNGY.KTT.QS.M.Y.S.                      53
APV-C  ..V.K..N.I....K..D———.I....A..V.—..V..VL.MLAAVG.G..FVV..R.AAPKF.-M.MN..N.K....-.-F.LLKKKKKKKKK      55
bRSV   AK.NQ.L.FIRR.DEL.H—SVDVG.ST.NVV.TTI..V.V.VILML.A.GLLFYC.TKST.IMLGKDQ...IN.LS.S————————K.           57
hRSV   .K.NQ.L.FIRR.DEL.H—NVNTG.ST.NIM.TTI..V.I.VLLSL.AIGLLLYC.AKNT.VTLSKDQ...IN.IA.S————————K.           57
PVM    H..NQTRTFFKA.DQL.DLSENREN.NLNKSY.LTTLLFVVH.III.AVIGFILYKVLK———MIRDNK.KSKSTP.LT————————VLS           53
```

Fig. 3, contd.

L polymerase RAP PCR fragment 8

```
00-1 fragment 8 --------TVNVYLPDSYLKGVISFSETNAIGSCLLKRPYLKNDNTAKVAIENPVIEHVRLKNAVNSKMKISDYK-----IVEPVNMQHE 77
APV-A           ME-ISNESV.....V.N...I.D.Y..H..MT.....Q..RALFK.LTISRE.R-----V...LMI.K. 84
bRSV            MDTLIHENST....T.....C..L..Y..DG.....Y.NIISRQK.L...IN..KLSIIQSFVTK.NKGELGLE..TYF.SL 90
hRSV            MDPIINGNSA....T.G.....C..L..YIFNG.....Y.NLISRQ..L...MN..KLNITQSL..K.HKGEIKLE..TYF.SL 90

00-1 fragment 8 IM--KNVHSCEL-----TLLKQFLTRSKNISTLKLNMICDWLQLK----------STSDDTSILSFIDVEFI---------- 13
APV-A           LL--.VAAGAR.-----KK..KW.G...D..EV..K.VT...K.S----------Q.PGRGK.IDR.Q..NL---------- 13
bRSV            L.TY.SLSTS..ITTT..F.KIIR.AIE..DV.VYA.LNK.G..EKGKVDRC----DDTN.TLSNIVRDNILSVISDNTPSTKKFNNSSCK 17
hRSV            L.TY.SMT.S.QIATTN...KIIR.AIE..DV.VYA.LNK.G..EKDKIKSNNGQDE.NSV.TTI.KDDILSAVKDNQSHLKADKNHSTK 18

00-1 fragment 8 ----------------PSWVSNWFSNWYNLNKLILEFRKEEVIRTGSIL--CRSLGKLVFVVSSYGCIVKSNKSKRVSFTTYNQLL 20
APV-A           ----------------.D.LEH..DS.LI..DV.QSY.CL..SQ.SA..--RK.SLNFF.A...F...II.R..R.IC.C..... 20
bRSV            PDQPIKTTILCKLLSSMSHP.T.LIH..NLYTK..DILTQY.TN.ARNH.Y..IDT.T..EFQ.ILNQ.....YHK.L.KITIT....F. 26
hRSV            QKDTIKTTLLKKLMCSMQHP...LIH..NLYTK..NILTQY.SN..KNH.FT.IDNQT.SGFQ.ILNQ.....YHKEL..ITVT....F. 27

00-1 fragment 8 TWKDVMLSRFNAWFCIWVSNSLNENQEGVGLRSNL-------Q                                              23
APV-A           ....LA.....L.V....C..SA.D.L....K.VGELLNR                                              24
bRSV            ....IS...L.VCMIT.I..C..TLNKSL...C                                                      30
hRSV            ....IS...L.VCLIT.I..C..TLNKSL.                                                         30
```

L polymerase RAP-PCR fragment 9/10

```
00-1 fragment 9/10 --KLVDKITSDQHIFSPDKIDMLTLGKMLMP---TIKGQKTDQ-----FLNKRENYFHGNNLIESLSAALAXHWCGILTEQC 72
APV-A              -F.S.R..VT.....N..H..LVM...L.L.--.VRSNINNN-------KPAT..F.N...IV.A.TSC..C...TV.ILLT 72
bRSV               -ICKLNQVIQK..M.L....SLSQYVELFLSNK.L.NSPHISSNLVLVH.MSD..LHKYV-----..TN..G..IM.IQLMK 76
hRSV               DIHKLKQVIQK..M.L....SLTQYVELFLSNK.L.SGSHVNSNLILAH.ISD...NTYI-----..TN..G..IL.IQLMK 77

00-1 fragment 9/10 IENNIFKKDWGDGFISDHAFMDFKIFLCVFKTKLLC                                                 10
APV-A              T..S..Q.E.....T....IN.TW..MS...Y...HW                                                 11
bRSV               DSKG..E....E.Y.T..M.L.INV.FDAY..Y.                                                    11
hRSV               DSKG..E....E.Y.T..M.INL.V.FNAY..Y                                                     11
```

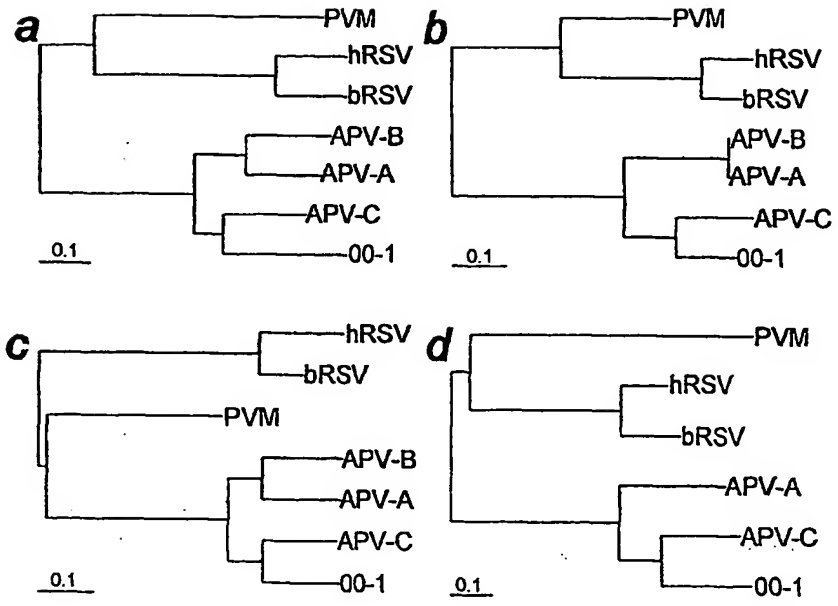

a
PVM
hRSV
bRSV
APV-B
APV-A
APV-C
00-1
0.1
b
PVM
hRSV
bRSV
APV-B
APV-A
APV-C
00-1
0.1
c
hRSV
bRSV
PVM
APV-B
APV-A
APV-C
00-1
0.1
d
PVM
hRSV
bRSV
APV-A
APV-C
00-1
0.1

Fig. 4

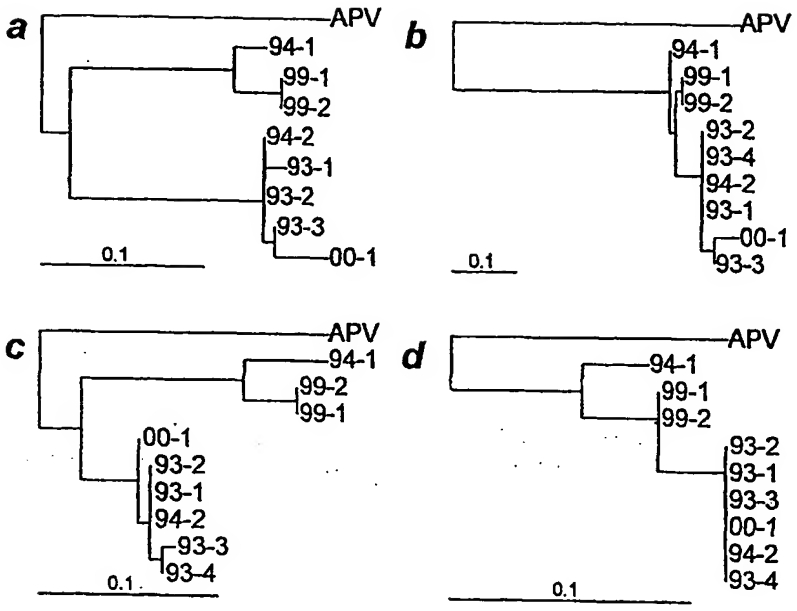

a
APV
94-1
99-1
99-2
94-2
93-1
93-2
93-3
00-1
0.1
b
APV
94-1
99-1
99-2
93-2
93-4
94-2
93-1
00-1
93-3
0.1
c
APV
94-1
99-2
99-1
00-1
93-2
93-1
94-2
93-3
93-4
0.1
d
APV
94-1
99-1
99-2
93-2
93-1
93-3
00-1
94-2
93-4
0.1

Fig. 5

Fig. 6A

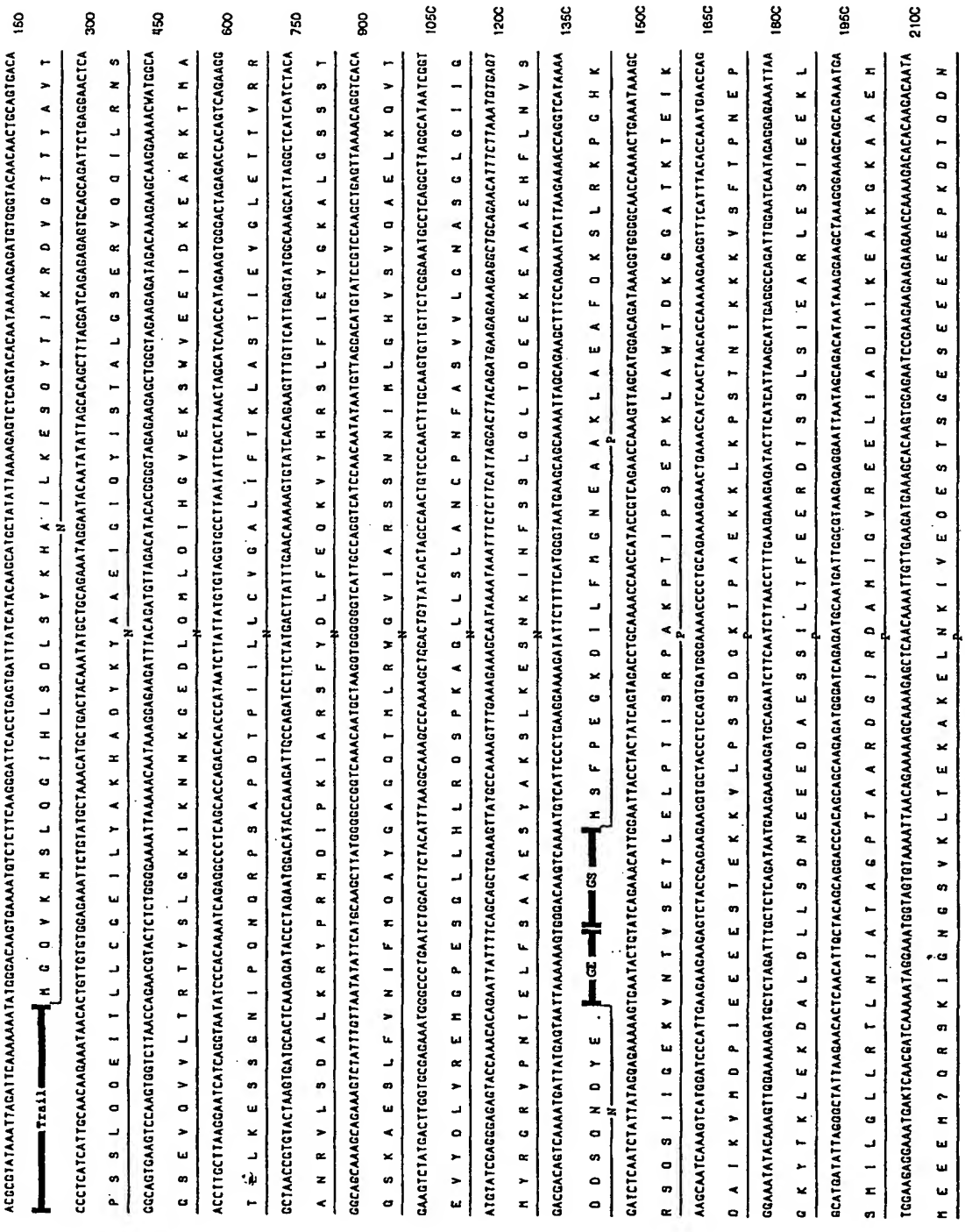


Fig. 6A, contd.

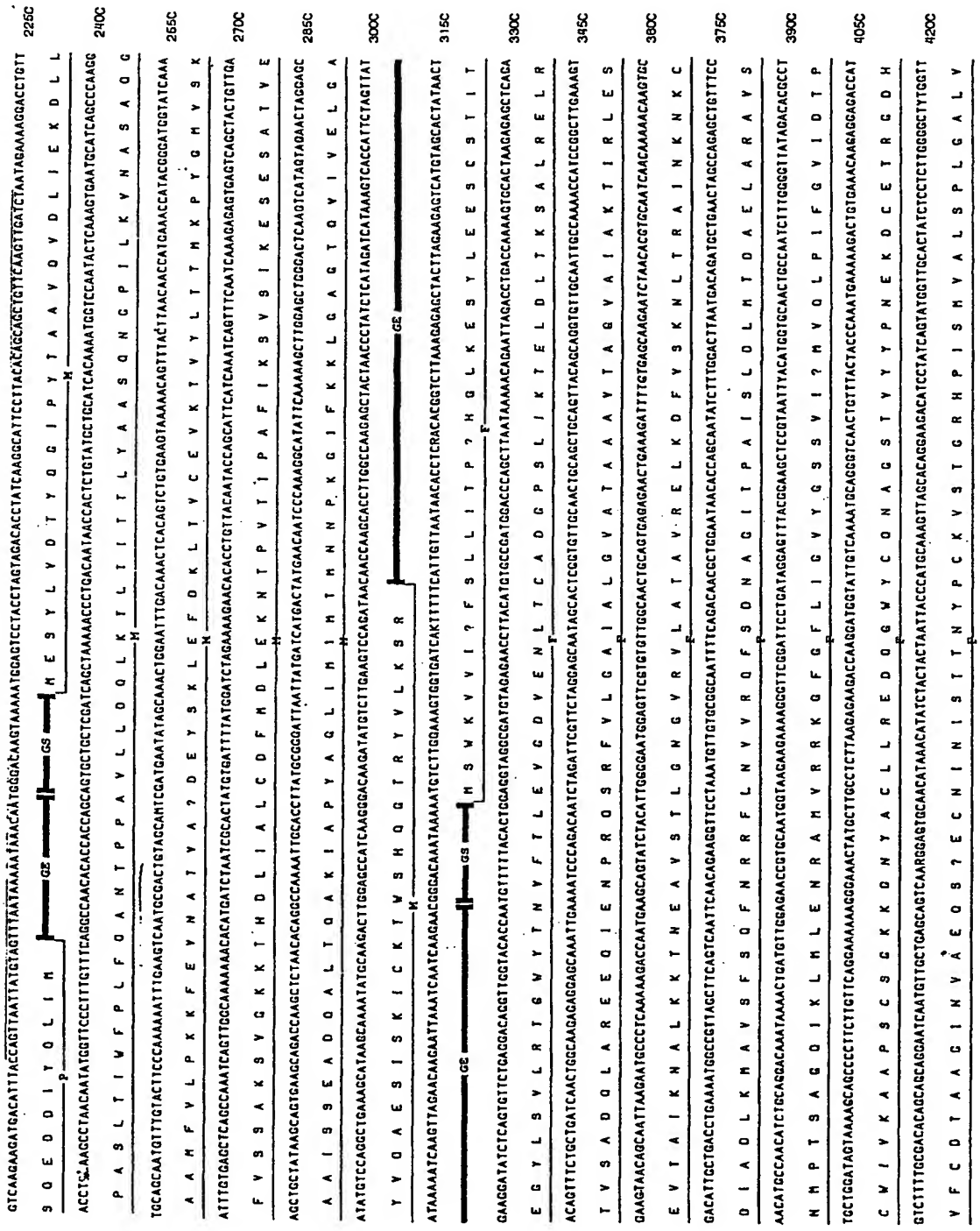
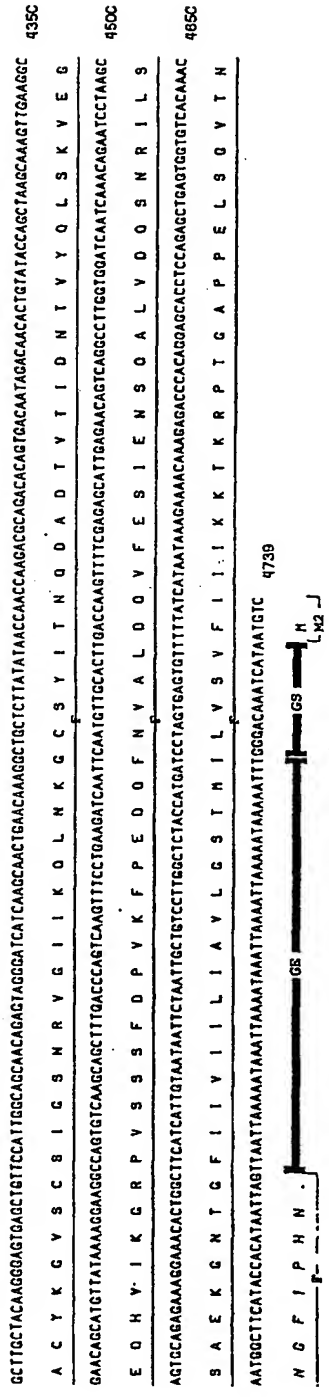


Fig. 6A, contd.



```
CAAGAAAAAAACTGTTCCACTGTTAATGTCTATCTTCCTGACTCATATCTTAAAGGAGTGATTTCCTTTAGTGAGACTAATGCAATTGGTTCATGTCTCTTAAAAAGACCTTACCTAAAAAATGACAACACTGCAAAAGTTGCCATAGAG 160

  Q  E  K  N  C  S  T  V  N  V  Y  L  P  D  S  Y  L  K  G  V  I  S  F  S  E  T  N  A  I  G  S  C  L  L  K  R  P  Y  L  K  N  D  N  T  A  K  V  A  I  E

AATCCTGTTATCGAGCATGTTAGACTCAAAAATGCAGTCAATTCTAAGATGAAAATATCAGATTACAAGATAGTAGAGCCAGTAAACATGCAACATCAAATTATGAAGAATGTACACAGTGTGAGCTCACATTATTAAAACAGTTTTTA 300

  N  P  V  I  E  H  V  R  L  K  N  A  V  N  S  K  H  K  I  S  D  Y  K  I  V  E  P  V  N  M  Q  H  E  I  M  K  N  V  H  S  C  E  L  T  L  L  K  Q  F  L

ACAAGGAGTAAAAATATTAGCACTCTCAAATTAAATATGATATGTATTGCTGCAGTTAAAGTCTACATCAGATGATACCTCAATCCTAAGTTTTATAGATGTAGAATTTATACCTAGCTGGGTAAGCAATTGGTTTAGTAATTGGTAC 460

  T  R  S  K  N  I  S  T  L  K  L  N  H  I  C  D  W  L  Q  L  K  S  T  S  D  D  T  S  I  L  S  F  I  D  V  E  F  I  P  S  W  V  S  N  W  F  S  N  W  Y

AATCTCAACAAGTTGATTCTGGAATTCAGGAAAGAAGAAGTAATAAGAACTGGTTCAATCTTGTGTAGGTCATTGGGTAAATTAGTTTTTGTTGTATCATCATATGGATGTATAGTCAAGAGCAACAAAGCAAAAGAGTGAGCTTCTTC 600

  N  L  N  K  L  I  L  E  F  R  K  E  E  V  I  R  T  G  S  I  L  C  R  S  L  G  K  L  V  F  V  V  S  S  Y  G  C  I  V  K  S  N  K  S  K  R  V  S  F  F

ACATACAATCAACTGTTAACATGGAAAGATGTGATGTTAAGTAGATTCAATGCAAATTTTTGTATATATGGGTAAGCAACAGTCTGAATCAAAATCAAGAAGGGGTAGGGTTGAGAAGTAATTTGCAAGGCATATTAACTAATAAGCTATAT 760

  T  Y  N  Q  L  L  T  W  K  D  V  M  L  S  R  F  N  A  N  F  C  I  W  V  S  N  S  L  N  E  N  Q  E  G  V  G  L  R  S  N  L  Q  G  I  L  T  N  K  L  Y

GAAACTGTAGATTATATGCTTAGTTTATGTT 781

  E  T  V  D  Y  M  L  S  L  C
```

Fig. 6B

```
ATAAGCTAGTAGATAAGATAACTTCTGATCAACATATCTTCAGTCCAGACAAAATAGATATGTTAACACTGGGGAAAATGCTCATGCCCACTATAAAAGGTCAGAAAACAGATCAGTTCCTGAACAAGAGAGAGAATTATTTCCATGGGA 150

  K  L  V  D  K  I  T  S  D  Q  H  I  F  S  P  D  K  I  D  M  L  T  L  G  K  M  L  M  P  T  I  K  G  Q  K  T  D  Q  F  L  N  K  R  E  N  Y  F  H  G

ATAATCTTATTGAGTCTTTGTCAGCAGCGTTAGCATGTCATTGGTGTGGGATATTAACAGAAAATAATATTTTCAAGAAAGACTGGGGTCACGGGTTCATATCGGATCATGCTTTTATGGACTTCAAAATATTCCTAT 300

N  N  L  I  E  S  L  S  A  A  L  A  C  H  W  C  G  I  L  T  E  Q  C  I  E  N  N  I  F  K  K  D  W  G  D  G  F  I  S  D  H  A  F  M  D  F  K  I  F  L

QTGTCTTTAAAACTAAACTTTTATGTA 327

C  V  F  K  T  K  L  L  C
```

Fig. 6C

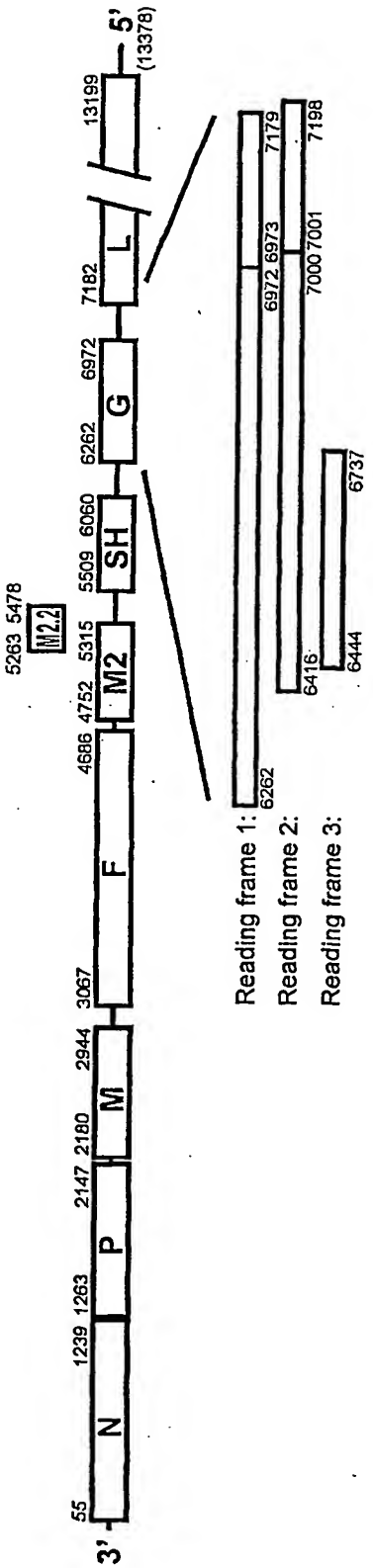

3'
55
N
1239
1263
P
2147
2180
M
2944
3067
F
4686
4752
M2
5315
M2.2
5263
5478
SH
5509
6060
G
6262
6972
L
7182
13199
5'
(13378)
Reading frame 1:
6262
6972
6973
7000
7001
7179
7198
Reading frame 2:
6416
6444
Reading frame 3:
6737

Fig. 7

Fig. 8

```
                                                                50
HMPV   MSLQGIHLSDLSYKHAILKESQYTIKRDVGTTTAVTPSSLQQEITLLCGE
APVC   ......Q...............................R.VS.....
APVB   ...ES.R....E......D.....R....A...I...E..PKVST...M
APVA   ...ES.R....E......ED.....R....A...I...E..PQVST...M
HRSVA  .A.SKVK.N.TLN.DQL.SS.K...Q.ST.DSIDTPNYDV.KH.NK...M
HRSVB  .A.SKVK.N.TLN.DQL.SS.K...Q.ST.DNIDTPNYDV.KHLNK...M
BRSV   .A.SKVK.N.TFN.DQL.ST.K...Q.ST.DNIDIPNYDV.KHLNK...M
PVM    ...DRLK.N.V.N.DSL.SNCK.SVT.ST.DV.S.SGHAM.KALARTL.M
                                                               100
HMPV   ILYAKHADYKYAAEIGIQYISTALGSERVQQILRNSGSEVQVVLTRTYSL
APVC   ......T..SH...V.M..V..T..A..T....K.......A...K....
APVB   ..F......EP..QV.M........ADKT....KS......G.M.KIVT.
APVA   V.F...T..EP...V.M........AD.T....K.......G.M.KIVT.
HRSVA  L.ITED.NH.FTGL..ML.AMSR..R.DTIK...DA.YH.KANGVDVTTH
HRSVB  L.ITED.NH.FTGL..ML.AMSR..R.DTIK..KDA.YH.KANGVDITTY
BRSV   L.ITED.NH.FTGL..ML.AMSR..R.DTLK..KDA.YQ.RANGVDVITH
PVM    F.LTAFNRCEEV....L..AMSL..RDDSIK...EA.YN.KC.D.QLKDF
                                                               150
HMPV   GKIKNNKGEDLQMLDIHGVEKSWVEEIDKEARKTMATLLKESSGNIPQNQ
APVC   ..G..S...E..........R..I..V.........SAT.DN..P.....
APVB   PAEGPIR--KREV.N..DIGPA.ADNVERT..E..SLMV..K-AQ..K..
APVA   SAEGSVR--KREV.N..D.GVG.ADDVERTT.EA.GAMVR.K-VQLTK..
HRSVA  RQDI.G.EMKFEV.TLASLTTEIQIN.EI.S..SYKKM...M-.EVAPEY
HRSVB  RQDI.G.EMKFEV.TLSSLTSEIQVN.EI.S..SYKKM...M-.EVAPEY
BRSV   RQDV.G.EMKFEV.TLVSLTSEVQGN.EI.S..SYKKM...M-.EVAPEY
PVM    TIKLQG.EYKI.V...V.IDAANLADLEIQ..GVV.KE..TG-ARL.D.R
                   A                                   200
HMPV   RPSAPDTPIILLCVGALIFTKLASTIEVGLETTVRRANRVLSDALKRYPR
APVC   ...S..A.......I..........................A........N.....F..
APVB   K...L.A.V....I...........V......AI...S......IS....
APVA   K...L.A.V....I...........V......AI...S......IS....
HRSVA  .HDS..CGM.I..IA..VI....AGDRS..TAVI....N..KNEM...KG
HRSVB  .HDS..CGM.I..IA..VI....AGDRS..TAVI....N..KNEI...KG
BRSV   .HDS..CGM.V...A..VI....AGDRS..TAVI....N..RNEM...KG
PVM    .HD...CGV.V..IA..VVS...AGDRG..DAVE...LN..KAEKA...N
                                                               250
HMPV   MDIPKIARSFYDLFEQKVYHRSLFIEYGKALGSSSTGSKAESLFVNIFMQ
APVC   I.................Y...............................
APVB   ....R..K..FE...K...Y.N...........T.S..RM..........
APVA   ....R..K..FE...K...Y.N...........T....RM..........
HRSVA  LLPKD..N...EV..KHPHFIDV.VHF.I.QS.TRG..RV.GI.AGL..N
HRSVB  LIPKD..N...EV..KHPHLIDV.VHF.I.QS.TRG..RV.GI.AGL..N
BRSV   LIPKD..N...EV..KYPHYIDV.VHF.I.QS.TRG..RV.GI.AGL..N
PVM    .EVKQ..E.......R.P.YIDV..TF.L.QS.VRG...V.G..SGL..N
          B                                        C   300
HMPV   AYGAGQTMLRWGVIARSSNNIMLGHVSVQAELKQVTEVYDLVREMGPESG
APVC   ..................................................
APVB   ..........R..V...................R..S.......K......
APVA   .....................................R..S.......K......
HRSVA  .....V.......L.K.VK......A....ME..V...EYAQKL.G.A.
HRSVB  ...S..V......L.K.VK......A....ME..V...EYAQKL.G.A.
BRSV   ......V......L.K.VK......A....ME..V...EYAQKL.G.A.
PVM    ......V......IL.K.VK......A....ME..V...EYAQKO.G.A.
                                                               350
HMPV   LLHLRQSPKAGLLSLANCPNFASVVLGNASGLGIIGMYRGRVPNTELFSA
APVC   ......N.........................L.............A.
APVB   .................TS............A.........K..A..L.....
APVA   .................T.............A.........K..A..L...A.
HRSVA  FY.ILNN...S....TQF.H.S........A....M.E...TPR.QD.YD.
HRSVB  FY.ILNN...S....TQF...S........A....M.E...TPR.QD.YD.
BRSV   FY.ILNN...S....TQF...S........A....M.E...TPR.QD.YD.
PVM    FY.I.NN...S....T.....T........A......S.K.APR.R...D.
                                                       395
HMPV   AESYAKSLKESNKINFSSLGLTDEEKEAAEHFLNVSDDS-QNDYE
APVC   .....R................E.......N...INEEG-.....
APVB   .....R.........LAA....ED.R...TSY.GGDE.K-SQKF.
APVA   .....RT.R.N....LAA.....D.R...TSY.GGD.ER-SSKF.
HRSVA  .KA..EQ...NGV..Y.V.D..A..L..IK.Q..PK.N--DVEL-
HRSVB  .KA..EQ...NGV..Y.V.D..A..L..IKNQ..PKE.--DVEL-
BRSV   .KA..EQ...NGV..Y.V.D..T..L..IKNQ..PK.N--DVEL-
PVM    .KD..ER..DN.V..Y.A.N..A..R.LISQQ..IV..TPDD.I-
```

Fig. 9

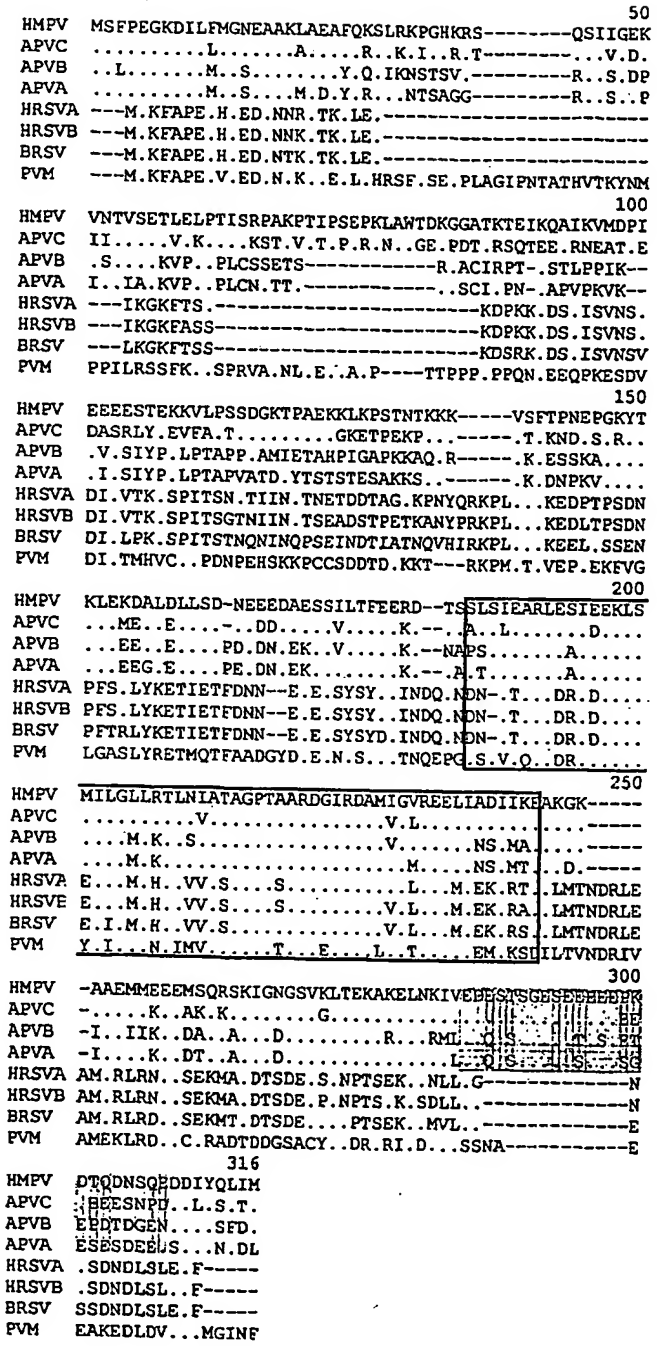

50
HMPV MSFPEGKDILFMGNEAAKLAEAFQKSLRKPGHKRS--------QSIIGEK
APVC .....L.....A.....R..K.I..R.T--------...V.D.
APVB ..L.....M..S.....Y.Q.IKNSTSV.---------R..S.DP
APVA .....M..S....M.D.Y.R...NTSAGG---------R..S..P
HRSVA ---M.KFAPE.H.ED.NNR.TK.LE.----------
HRSVB ---M.KFAPE.H.ED.NNK.TK.LE.----------
BRSV ---M.KFAPE.H.ED.NTK.TK.LE.----------
PVM ---M.KFAPE.V.ED.N.K..E.L.HRSF.SE.PLAGIPNTATHVTKYNM
100
HMPV VNTVSETLELPTISRPAKPTIPSEPKLAWTDKGGATKTEIKQAIKVMDPI
APVC II.....V.K....KST.V.T.P.R.N..GE.PDT.RSQTEE.RNEAT.E
APVB .S....KVP..PLCSSETS----------R.ACIRPT-.STLPPIK--
APVA I..IA.KVP..PLCN.TT.----------..SCI.PN-.APVPKVK--
HRSVA ---IKGKFTS.----------KDPKK.DS.ISVNS.
HRSVB ---IKGKFASS----------KDPKK.DS.ISVNS.
BRSV ---LKGKFTSS----------KDSRK.DS.ISVNSV
PVM PPILRSSFK..SPRVA.NL.E..A.P----TTPPP.PPQN.EEQPKESDV
150
HMPV EEEESTEKKVLPSSDGKTPAEKKLKPSTNTKKK-----VSFTPNEPGKYT
APVC DASRLY.EVFA.T.....GKETPEKP...-----.T.KND.S.R..
APVB .V.SIYP.LPTAPP.AMIETAHPIGAPKKAQ.R-----.K.ESSKA....
APVA .I.SIYP.LPTAPVATD.YTSTSTESAKKS..------.K.DNPKV....
HRSVA DI.VTK.SPITSN.TIIN.TNETDDTAG.KPNYQRKPL...KEDPTPSDN
HRSVB DI.VTK.SPITSGTNIIN.TSEADSTPETKANYPRKPL...KEDLTPSDN
BRSV DI.LPK.SPITSTNQNINQPSEINDTIATNQVHIRKPL...KEEL.SSEN
PVM DI.TMHVC..PDNPEHSKKPCCSDDTD.KKT---RKPM.T.VEP.EKFVG
200
HMPV KLEKDALDLLSD-NEEEDAESSILTFEERD--TSSLSIEARLESIEEKLS
APVC ...ME..E....-..DD.....V.....K.--..A..L.....D....
APVB ...EE..E....PD.DN.EK..V.....K.--NAPS.....A.....
APVA ...EEG.E....PE.DN.EK.....K.--.A.T.....A.....
HRSVA PFS.LYKETIETFDNN--E.E.SYSY..INDQ.NDN-.T...DR.D.....
HRSVB PFS.LYKETIETFDNN--E.E.SYSY..INDQ.NDN-.T...DR.D....
BRSV PFTRLYKETIETFDNN--E.E.SYSYD.INDQ.NDN-.T...DR.D....
PVM LGASLYRETMQTFAADGYD.E.N.S...TNQEPG.S.V.Q..DR.....
250
HMPV MILGLLRTLNIATAGPTAARDGIRDAMIGVREELIADIIKEAKGK-----
APVC .....V.....V.L.....-----
APVB ....M.K..S.....V.....NS.MA.....-----
APVA ....M.K.....M.....NS.MT..D.-----
HRSVA E...M.H..VV.S....S.....L...M.EK.RT..LMTNDRLE
HRSVB E...M.H..VV.S....S.....V.L...M.EK.RA..LMTNDRLE
BRSV E.I.M.H..VV.S.....V.L...M.EK.RS..LMTNDRLE
PVM Y.I...N.IMV.....T...E....L..T.....EM.KSDILTVNDRIV
300
HMPV -AAEMMEEEMSQRSKIGNGSVKLTEKAKELNKIVEEESISGESEEEEDHK
APVC -.....K..AK.K.....G.....EE
APVB -I..IIK..DA..A...D.....R...RML..Q.S...T.S.ET
APVA -I....K..DT..A...D.....L..Q.S...T.S..N
HRSVA AM.RLRN..SEKMA.DTSDE.S.NPTSEK..NLL.G----------N
HRSVB AM.RLRN..SEKMA.DTSDE.P.NPTS.K.SDLL..----------N
BRSV AM.RLRD..SEKMT.DTSDE....PTSEK..MVL..----------E
PVM AMEKLRD..C.RADTDDGSACY..DR.RI.D...SSNA----------E
316
HMPV DTQDNSQEDDIYQLIM
APVC .EESNPD..L.S.T.
APVB EEDTDGEN....SFD.
APVA ESESDEELS...N.DL
HRSVA .SDNDLSLE.F-----
HRSVB .SDNDLSL..F-----
BRSV SSDNDLSLE.F-----
PVM EAKEDLDV...MGINF

Fig. 10

```
                                                                      50
HMPV  MESYLVDTYQGIPKTAAVQVDLIEKDLLPASLTIWFPLFQANTPPAVLLD
APVC  ..........V.....T..V...Q...R..V.V....T....T...E
APVB  ....II.....V.....T..V...NN..K..V......SS..AP....
APVA  ....II.....V.....T.......SN..T..V......SS..AP....
HRSVA ..T.VNKLHE.ST.....YNVL...DD.......V.M..SSM.ADL.IK
HRSVB ..T.VNKLHE.ST.....YNVL...DD.......V.M..SSV.ADL.IK
BRSV  ..T.VNKLHE.ST.....YNV....DD.......V.M..SSISADL.IK
PVM   ..A...EM.H.V.....LN.V..HSANI...V.I.M..TSL.KNSVM.
                                                                     100
HMPV  QLKTLTITTLYAASQNGPILKVNASAQGAAMSVLPKKFEVNATVALDEYS
APVC  ..........T.....................A...S.D.S.S....D..
APVB  .....S...Q.TV.PE..V.Q...T.......A.....S.S.AA......
APVA  .....S...Q.T..PE..V.Q...A.......A.....A.S.A.......
HRSVA E.ANVN.LVKQISTPK..S.R.MINSRS.VLAQM.S..TIC.N.S...R.
HRSVB E.ASIN.LVKQISTPK..S.R.TINSRS.VLAQM.SN.IIS.N.S...R.
BRSV  E.INVN.LVRQISTLK..S..IMINSRS.VLAQM.S..TIS.N.S...R.
PVM   L.HDV.VICTQISTVH..MI..DL.SSN.GLATM.RQ.LI..II...DWG
                                                                     150
HMPV  KLEFDKLTVCEVKTVYLTTMKPYGMVSKFVSSAKSVGKKTHDLIALCDFM
APVC  ..........L.A.............N...A.............L
APVB  ..D.GV....D.RA.....L.........I.TNMNT..R...........I
APVA  R...GT....D.RSI....L.........IMTDVR...R...........I
HRSVA ..AY.VT.P..I.ACS..CL.SKN.LTTVKDLTMKTLNP...I....E.E
HRSVB ..AY.VT.P..I.ACS..CL.VKS.LTTVKDLTMKTFNP..EI....E.E
BRSV  ..AY.IT.P..I.ACS..CL.VKN.LTTVKDLTMKTFNP..EI....E.E
PVM   NMDYEVPVAFDK.SFCV.IL..KN.LYTVP.ITP-TNRP..E...V.S.H
                                                                     200
HMPV  DLEKNTPVTIPAFIKSVSIKESESATVEAAISSEADQALTQAKIAPYAGL
APVC  ....GV......Y...................G.....I...R.......
APVB  .M.RGI......Y..A....D...........G.....I...R.......
APVA  .I..GV.I....Y..A....D...........G.....I...R.......
HRSVA NIVTSKK.I..TYLR.I.VRNKDLN.L.NITTT.FKN.I.N...I..S..
HRSVB NIMTSKR.I..TYLRPI.V.NKDLNSL.NIATT.FKN.I.N...I.....
BRSV  NIMTSKR.V..T.LR.INV.AKDLDSL.NIATT.FKN.I.N...I.....
PVM   NRVTLKSFN..V..RALY.RQQGLDS..Q....DV.H.I.T.RV......
                                                                     250
HMPV  IMIMTMNNPKGIFKKLGAGTQVIVELGAYVQAESISKICKTWSHQGTRYV
APVC  ..................V................R..RN.........
APVB  .LL.A.........R.............P......LG......N..R...I
APVA  .L.................M.......P......LG......N..R....
HRSVA LLVI.VTDN..A..YIKPQS.F..D....LEK...YYVTTN.K.TA..FA
HRSVB VLVI.VTDN..A..YIKPQS.F..D....LEK...YYVTTN.K.TA..FS
BRSV  VLVI.VTDN..A..YIKPQS.F..D....LEK...YYVTTN.K.TA.KFS
PVM   TLVINITST..A..L.K..S.ILA...P.LTQV.LHDVIMN.K.T..S.I
          258
HMPV  LKSR----
APVC  ....----
APVB  ....----
APVA  .R..----
HRSVA I.PMED--
HRSVB I.PLED--
BRSV  I.PIED--
PVM   ...SSTSG
```

Fig. 11

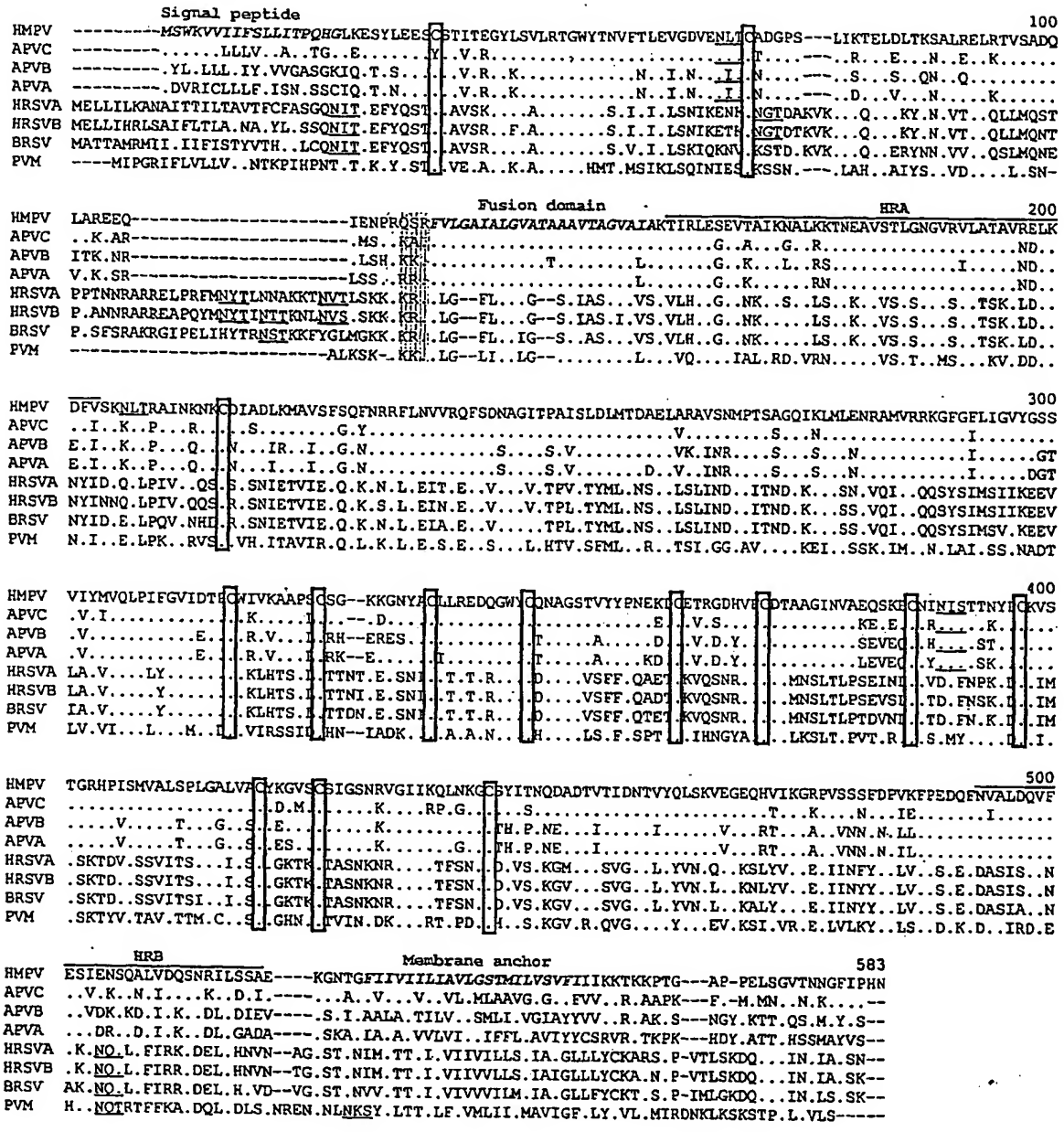

Signal peptide
Fusion domain
HRA
HRB
Membrane anchor
HMPV
APVC
APVB
APVA
HRSVA
HRSVB
BRSV
PVM

Fig. 12

A

```
                 #       #     #                                    50
HMPV  MSRKARCKYEVRGKCNRGSECKFNHNYWSWPDRYLLIRSNYLLNQLERNT
APVC  ..........................................L.............
APVB  ..GRN..R..T..R.....S.T.........HV..V.A..M....V...
APVA  ...RN..R..I........S.T.........HV..V.A..M........
HRSVA ...RN...F.I..H.LN.KR.H.S...FE..PHA..V.Q.FM..RI.KSM
HRSVB ...RN...F.I..H.LN.RR.HYS...FE..PHA..V.Q.FM..KI.KSM
BRSV  ...RN.....I..H.LN.KK.H.S...FE..PHA..V.Q.FM..KI.KSM
PVM   ..VR-...F..Q.F.S..RN..YS.K..E..LKT.ML.Q..M..RIY.FL
                                                        # 100
HMPV  DRA-DGLSITSGAGREDRTQDFVLGSTNVVQGYIDDNQSITKAAACYSLH
APVC  ..S-....L......D..............N...N.EN....ST....Y
APVB  ..T-....L.................A....N..EG.AT...S......Y
APVA  ..T-....L.................A....N..EG.TT...S......Y
HRSVA .KSI.T..E....AEL...EEYA..VVG.LES..GSINN...QS..VAMS
HRSVB .KSI.T..E....AEL...EEYA..IVG.LES..GSINN...QS..VAMS
BRSV  ..NN.T..E....AEL...EEYA..VIG.LES.LGSINN...QS..VAMS
PVM   .TNT.AI.DV..FDAPQ..AEYA..TIG.LKS.LEKTNN...SI..G..I
                                                       150
HMPV  NIIKQLQEVEVRQARDNKLSDSKHVALHNLVLSYMEMS-KTPASLINNLK
APVC  ........TD........VD.................-...........
APVB  ........ND.KS...LMVD.P.....:........ID..-.N..N...S..
APVA  ........ND.KTS..SM.E.P........I...VD..-.N......S..
HRSVA KLLTE.NSDDIKKL...EELN.PKIRVY.T.I..I.SNR.NNKQT.HL..
HRSVB KLLIEINSDDIKKL...EEPN.PKIRVY.T.I..I.SNR.NNKQT.HL..
BRSV  KLLAEINNDDIKRL.NKEVPT.PKIRIY.T.I..IDSNKRNTKQT.HL..
PVM   TVLQN.DVGL.I....SNTE.TNYLRSC.TI...IDKIL.K-RQI.HI..
                                                       195
HMPV  RLPREKLKKLAKLIIDLSAGAE--NDSSYALQDSESTNQVQ----
APVC  K..K..........E....V.--...TA.M...ANSD-------
APVB  ...K........I..Q....S.GE.AN.NT..KGD.S.-------
APVA  ............I.LQ....P.SD.A.GNT..KGD.N.-------
HRSVA ...ADV...TI.NTL.IHKSITIN.PKESTVS.TNDHAKNNDTT-
HRSVB ...ADV...TI.NTL.IHKSIIIS.PKESTVN.QNDQTKNNDITG
BRSV  ...ADV...TI.NT..IHNEINGN.QGDIIVNEQNE---------
PVM   ...VGV.CN.IQSV.SIEEKINSSMKTE----------------
```

B

```
                                                        50
HMPV  ---------MTLHMP-CKTVKALIKCS--------EHGPVFITIEVDDMIW
APVC  ---------...QL.-..I.QT....G---------...LI.LKMKL...V.
APVB  ---------.PIVI.-..R.T.V.R.N---------TL.VCLFKRTYEHN.I
APVA  ---------.PVVI.-.RR.T.I...N---------AL.LCMVRKIY.YS.A
HRSVA MTMPKIMILPDKY.-.SITSI..TSRCRVTMYNQKNTLY.NQNNPNNHMY
HRSVB MTKPKIMILPDKY.-.SISSI..SSESMIATFNHKNILQ.NHNHL.NHQR
BRSV  MNNSNIIIFPEKY.-.SISSL...NENDVIVLSHQNVLDYLQFQYPCNMY
PVM   MQSDPICHLHRGEDKFFYENRM.RLPKYYPAILHKMYIIRVNRNLTYDGS
                                                        97
HMPV  THKDLKEA---L---SDGIVKSHTNIYNCYLENIEIIYVKAYLS----
APVC  .KNE.VDI---I---.TE...V.A..FK.R..D.......TF..----
APVB  NLG..I.E---V---ARM.IID.I.RKQ.NECRKDFEF.AV.T.YT--
APVA  SWS..I.E---V---ANMVLID.I.RKQ.VECRKDFEFIAI.T.YN--
HRSVA SPNQTFNE---IHWT.QELIDTIQ.FLQHLGIIED.YTIYILV.----
HRSVB LLNNIFDE---IHWTPKNLLDATQQFLQHLNIPED.YTIYILV.----
BRSV  SQNHMLDD---IYWT.QELIEDVLK.LHLSGIS.SKYVIYVLVL----
PVM   GPSTIID.GKSVVWNRVDVIACVKEALC.IEFSWNNQVIIDFDYSQAR
```

Fig. 13

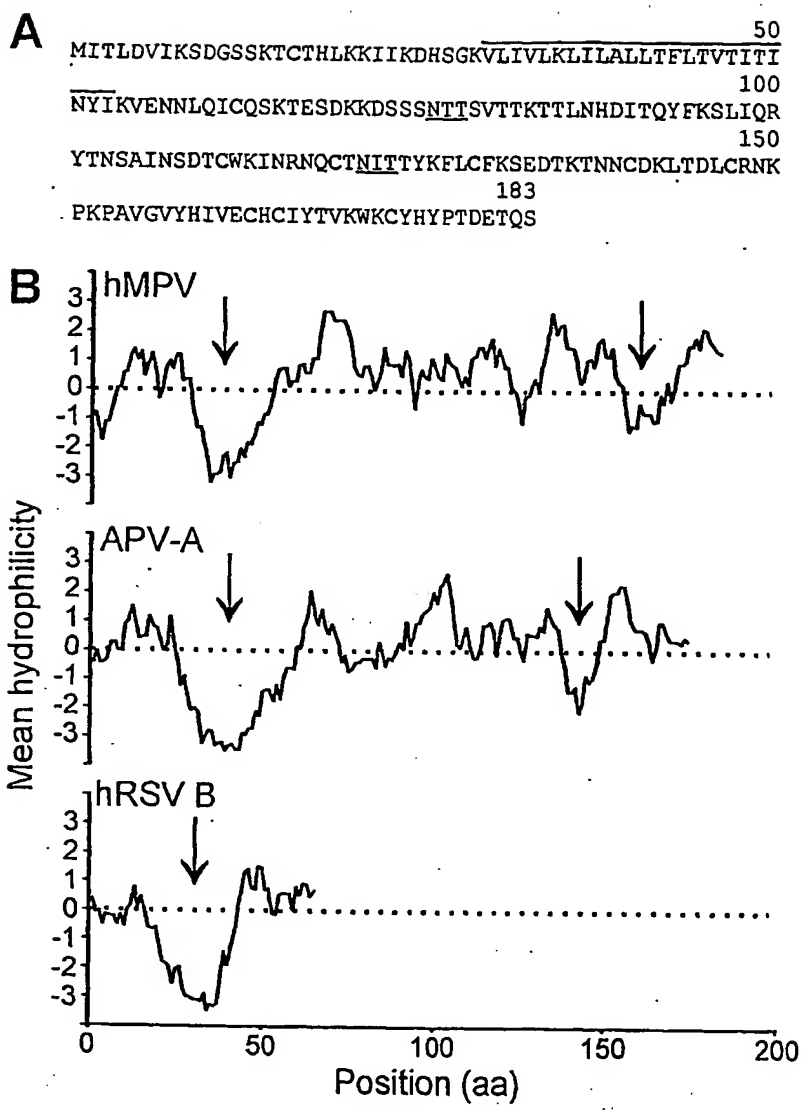

A
50
MITLDVIKSDGSSKTCTHLKKIIKDHSGKVLIVLKLILALLTFLTVTITI
100
NYIKVENNLQICQSKTESDKKDSSSNTTSVTTKTTLNHDITQYFKSLIQR
150
YTNSAINSDTCWKINRNQCTNITTYKFLCFKSEDTKTNNCDKLTDLCRNK
183
PKPAVGVYHIVECHCIYTVKWKCYHYPTDETQS
B
hMPV
APV-A
hRSV B
Mean hydrophilicity
3
2
1
0
-1
-2
-3
0
50
100
150
200
Position (aa)

Fig. 14

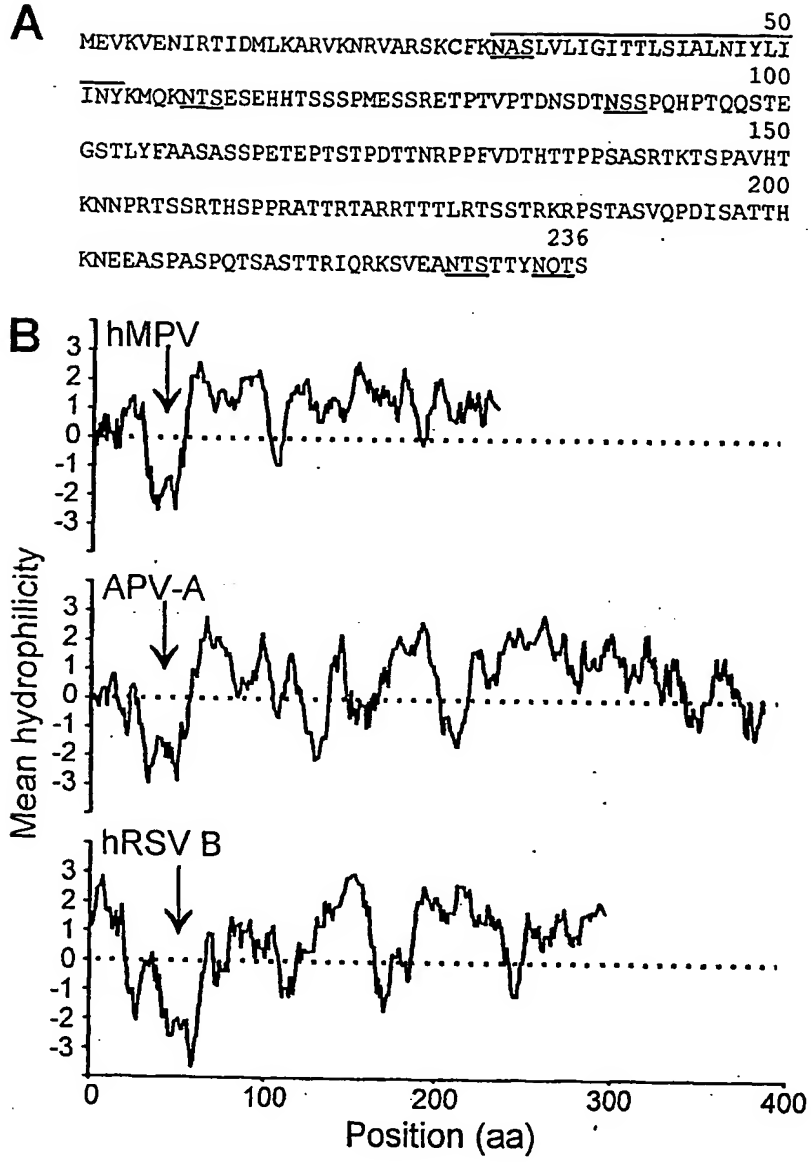

A
50
MEVKVENIRTIDMLKARVKNRVARSKCFKNASLVLIGITTLSIALNIYLI
100
INYKMQKNTSESEHHTSSSPMESSRETPTVPTDNSDTNSSPQHPTQQSTE
150
GSTLYFAASASSPETEPTSTPDTTNRPPFVDTHTTPPSASRTKTSPAVHT
200
KNNPRTSSRTHSPPRATTRTARRTTTLRTSSTRKRPSTASVQPDISATTH
236
KNEEASPASPQTSASTTRIQRKSVEANTSTTYNQTS
B
hMPV
APV-A
hRSV B
Mean hydrophilicity
3
2
1
0
-1
-2
-3
0
100
200
300
400
Position (aa)

Fig. 15

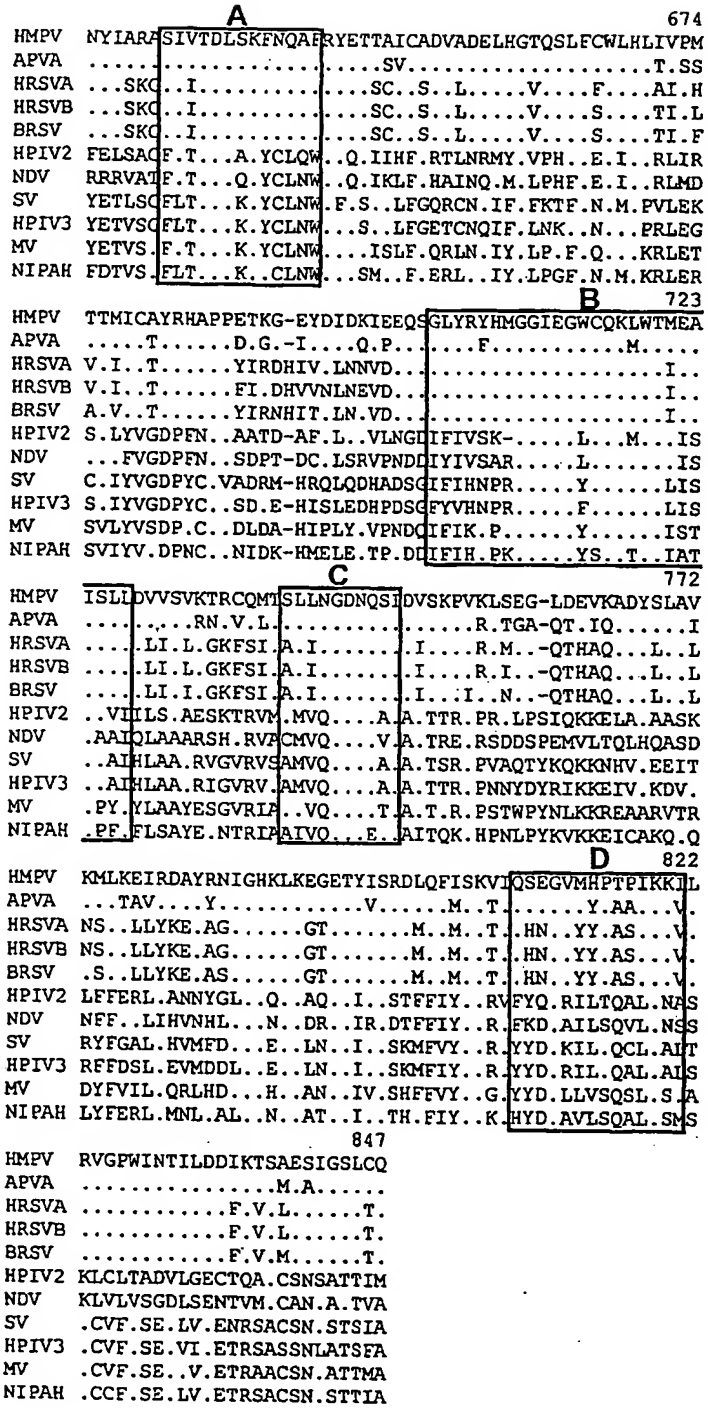
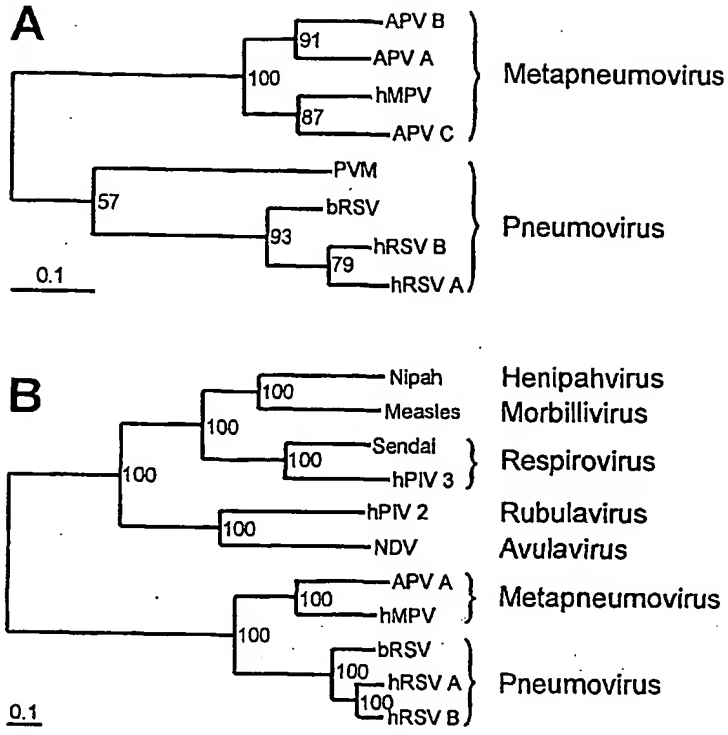

A
B
C
D
674
723
772
822
847
HMPV NYIARASIVTDLSKFNQAERYETTAICADVADELHGTQSLFCWLHLIVPM
APVA .....SV.....T.SS
HRSVA ...SKQ..I.....SC..S..L.....V....F....AI.H
HRSVB ...SKQ..I.....SC..S..L.....V....S....TI.L
BRSV ...SKQ..I.....SC..S..L.....V....S....TI.F
HPIV2 FELSAQF.T...A.YCLQW..Q.IIHF.RTLNRMY.VPH..E.I..RLIR
NDV RRRVATF.T...Q.YCLNW..Q.IKLF.HAINQ.M.LPHF.E.I..RLMD
SV YETLSQFLT...K.YCLNW.F.S..LFGQRCN.IF.FKTF.N.M.PVLEK
HPIV3 YETVSQFLT...K.YCLNW...S..LFGETCNQIF.LNK..N...PRLEG
MV YETVS.F.T...K.YCLNW....ISLF.QRLN.IY.LP.F.Q...KRLET
NIPAH FDTVS.FLT...K..CLNW...SM..F.ERL..IY.LPGF.N.M.KRLER
HMPV TTMICAYRHAPPETKG-EYDIDKIEEQSGLYRYHMGGIEGWCQKLWTMEA
APVA .....T.....D.G.-I....Q.P.....F.....M.....
HRSVA V.I..T.....YIRDHIV.LNNVD.....I..
HRSVB V.I..T.....FI.DHVVNLNEVD.....I..
BRSV A.V..T.....YIRNHIT.LN.VD.....I..
HPIV2 S.LYVGDPFN..AATD-AF.L..VLNGDIFIVSK-.....L...M...IS
NDV ...FVGDPFN..SDPT-DC.LSRVPNDDIYIVSAR.....L.....IS
SV C.IYVGDPYC.VADRM-HRQLQDHADSGIFIHNPR.....Y.....LIS
HPIV3 S.IYVGDPYC..SD.E-HISLEDHPDSGFYVHNPR.....F.....LIS
MV SVLYVSDP.C..DLDA-HIPLY.VPNDQIFIK.P.....Y.....IST
NIPAH SVIYV.DPNC..NIDK-HMELE.TP.DDIFIH.PK.....YS..T..IAT
HMPV ISLLDVVSVKTRCQMISLLNGDNQSIDVSKPVKLSEG-LDEVKADYSLAV
APVA ....RN.V.L.....R.TGA-QT.IQ.....I
HRSVA ....LI.L.GKFSI.A.I.....I....R.M..-QTHAQ...L..L
HRSVB ....LI.L.GKFSI.A.I.....I....R.I..-QTHAQ...L..L
BRSV ....LI.I.GKFSI.A.I.....I...I..N..-QTHAQ...L..L
HPIV2 ..VIILS.AESKTRVM.MVQ....A.A.TTR.PR.LPSIQKKELA.AASK
NDV .AAIQLAAARSH.RVACMVQ....V.A.TRE.RSDDSPEMVLTQLHQASD
SV ..AIHLAA.RVGVRVSAMVQ....A.A.TSR.PVAQTYKQKKNHV.EEIT
HPIV3 ..AIHLAA.RIGVRV.AMVQ....A.A.TTR.PNNYDYRIKKEIV.KDV.
MV .PY.YLAAYESGVRIP..VQ....T.A.T.R.PSTWPYNLKKREAARVTR
NIPAH .PF.FLSAYE.NTRIPAIVQ...E..AITQK.HPNLPYKVKKEICAKQ.Q
HMPV KMLKEIRDAYRNIGHKLKEGETYISRDLQFISKVIQSEGVMHPTPIKKIL
APVA ...TAV....Y.....V.....M..T.....Y.AA...V.
HRSVA NS..LLYKE.AG.....GT.....M..M..T..HN..YY.AS...V.
HRSVB NS..LLYKE.AG.....GT.....M..M..T..HN..YY.AS...V.
BRSV .S..LLYKE.AS.....GT.....M..M..T..HN..YY.AS...V.
HPIV2 LFFERL.ANNYGL..Q..AQ..I..STFFIY..RVFYQ.RILTQAL.NAS
NDV NFF..LIHVNHL...N..DR..IR.DTFFIY..R.FKD.AILSQVL.NSS
SV RYFGAL.HVMFD...E..LN..I..SKMFVY..R.YYD.KIL.QCL.AIT
HPIV3 RFFDSL.EVMDDL..E..LN..I..SKMFIY..R.YYD.RIL.QAL.AIS
MV DYFVIL.QRLHD...H..AN..IV.SHFFVY..G.YYD.LLVSQSL.S.A
NIPAH LYFERL.MNL.AL..N..AT..I..TH.FIY..K.HYD.AVLSQAL.SMS
HMPV RVGPWINTILDDIKTSAESIGSLCQ
APVA .....M.A.....
HRSVA .....F.V.L.....T.
HRSVB .....F.V.L.....T.
BRSV .....F.V.M.....T.
HPIV2 KLCLTADVLGECTQA.CSNSATTIM
NDV KLVLVSGDLSENTVM.CAN.A.TVA
SV .CVF.SE.LV.ENRSACSN.STSIA
HPIV3 .CVF.SE.VI.ETRSASSNLATSFA
MV .CVF.SE..V.ETRAACSN.ATTMA
NIPAH .CCF.SE.LV.ETRSACSN.STTIA

Fig. 16


A
APV B
APV A
hMPV
APV C
91
100
87
Metapneumovirus
PVM
bRSV
hRSV B
hRSV A
57
93
79
Pneumovirus
0.1
B
Nipah
Measles
Sendai
hPIV 3
hPIV 2
NDV
APV A
hMPV
bRSV
hRSV A
hRSV B
100
100
100
100
100
100
100
100
Henipahvirus
Morbillivirus
Respirovirus
Rubulavirus
Avulavirus
Metapneumovirus
Pneumovirus
0.1

A

Pos.,ORF	Stop	Non-coding sequence	Gene start	Start	Pos.,ORF
1,Le		ACGAGAAAAAAACGCGUAUAAAUUAGAUUCCAAAAAAAUAU.....	GGGACAAGUGAAA	AUG	55,N
1237,N	UAA	UUAAAAAAGU.....	GGGACAAGUCAAA	AUG	1263,P
2145,P	UAG	UUUAAUAAAAAUAAACAAU.....	GGGACAAGUAAAA	AUG	2180,M
2942,M	UAA	CAACCAAGCACCUUGGCCAAGAGCUACUAACCCUAUCUCAUAGAUCAUAAAGUCACCAUUCUAGUUAUAU AAAAAUCAAGUUAGAACAAGAAUUAAAUCAAUCAAGAAC.....	GGGACAAAUAAAA	AUG	3067,F
4684,F	UAG	UUAAUUAAAAAUAAAGUAAAUUAAAAUAAAUUAAAAUUAAAAAUAAAAAUUU.....	GGGACAAAUCAUA	AUG	4752,M2
5476,M2	UAG	UAAAAACACAUCAGAGU.....	GGGAUAAAUGACA	AUG	5509,SH
6058,SH	UAA	AUGUUAACACCAGAUUAGGAUCCAUCCAAGUCUGUUAGUUCAACAAUUUAGUUAUUUUAAAAAUAUUUUGA AAACAAGUAAGUUUCUAUGAUACUUCAUAAUAAUAAGUAAUAAUUAAUUGCUUAAUCAUCAUCACAACAU UAUUCGAAACCAUAACUAUUCAAUUUAAAAAGUAAAAAACAAUAACAU.....	GGGACAAGUAGUU	AUG	6262,G
6970,G	UAA	CAAAAAAUACAAAAUAACUCUAAGAUAAACCAUGCAGACACCAACAAUGGAGAAGCCAAAAGACAAUUCA CAAUCUCCCCAAAAAGGCAACAACACCAUAUUAGCUCUGCCCAAAUCUCCCUGGAAAAAACACUCGCCCA UAUACCAAAAAUACCACAACCACCCCAAGAAAAAAACUGGGCAAAACAACACCCAA.....	GAGACAAAUAACA	AUG	7182,L
13197,L	UGA	AAAAUGAUAAAAAUGAUAAAAUAGGUGACAACUUCAUACUAUUCCAAAGUAAUCAUUUGAUUAUGCAAUU AUGUAAUAGUUAAUUAAAAACUAAAAAUCAAAAGUUAGAAACUAACAACUGUCAUUAAGUUUAUUAAAAA UAAGAAAUUAUAAUUGGAUGUAUACGGUUUUUUUCUCGU			13378,Tr

B

```
hMPV Le: 3' UGCUCUUUUUUUGCGCAUAUUUAAUCUAAGGUUUUUUUAUACCCU
         |||||||||||||| |||||| ||   ||| ||     |||   |
hMPV Tr: 5' ACGAGAAAAAAAC CGUAUACAUCCAAUUAUAAUUUCUUAUUUUU

hMPV Tr: 5' ACGAGAAAAAAACCGUAUACAUCCAAUUAUAAUUUCUUAUUUUUA
         ||||||||||||||||| |||| |||| | |  | ||| ||||
APV  Tr: 5' ACGAGAAAAAAACCGUAUUCAUCAAAUUUUUAGCUUUUAGUUUUU

hMPV Le: 3' UGCUCUUUUUUUGCGCAUAUUUAAUCUAAGGUUUUUUUAU-ACCC
         |||||||||||||| | | ||  || ||| | |||||||| ||||
APV  Le: 3' UGCUCUUUUUUUGCGUA-AGUUCGUCCAAGAUCUUUUUAUUACCC
```

Fig. 17

Fig. 18a

Comparison of two prototypic hMPV isolates with APV-A and APV-C

DNA similarity matrices

N	00-1	99-1	APVC	APVA
00-1	1,000	0,862	0,757	0,660
99-1	---	1,000	0,757	0,663
APVC	---	---	1,000	0,656
APVA	---	---	---	1,000

P	00-1	99-1	APVC	APVA
00-1	1,000	0,811	0,677	0,588
99-1	---	1,000	0,674	0,593
APVC	---	---	1,000	0,584
APVA	---	---	---	1,000

M	00-1	99-1	APVC	APVA
00-1	1,000	0,865	0,766	0,695
99-1	---	1,000	0,773	0,707
APVC	---	---	1,000	0,705
APVA	---	---	---	1,000

F	00-1	99-1	APVC	APVA
00-1	1,000	0,838	0,706	0,662
99-1	---	1,000	0,716	0,655
APVC	---	---	1,000	0,685
APVA	---	---	---	1,000

M2-1	00-1	99-1	APVC	APVA
00-1	1,000	0,863	0,764	0,668
99-1	---	1,000	0,744	0,657
APVC	---	---	1,000	0,670
APVA	---	---	---	1,000

M2-2	00-1	99-1	APVC	APVA
00-1	1,000	0,861	0,648	0,486
99-1	---	1,000	0,675	0,486
APVC	---	---	1,000	0,463
APVA	---	---	---	1,000

SH	00-1	99-1	APVC	APVA
00-1	1,000	0,688	N.A.	0,421
99-1	---	1,000	N.A.	0,380
APVC	---	---	N.A.	N.A.
APVA	---	---	---	1,000

G	00-1	99-1	APVC	APVA
00-1	1,000	0,543	N.A.	0,262
99-1	---	1,000	N.A.	0,263
APVC	---	---	N.A.	N.A.
APVA	---	---	---	1,000

Fig. 18b

5'L	00-1	99-1	APVC	APVA
00-1	1,000	0,835	N.A.	0,596
99-1	---	1,000	N.A.	0,605
APVC	---	---	N.A.	N.A.
APVA	---	---	---	1,000

5'L: only the first 1500 nucleotides of 99-1 were available.
N.A.: sequence not available.

Protein similarity matrices

N 00-1	99-1	APVC	APVA	
00-1	1,000	0,949	0,880	0,685
99-1	---	1,000	0,883	0,682
APVC	---	---	1,000	0,700
APVA	---	---	---	1,000

P 00-1	99-1	APVC	APVA	
00-1	1,000	0,860	0,683	0,552
99-1	---	1,000	0,676	0,549
APVC	---	---	1,000	0,528
APVA	---	---	---	1,000

M 00-1	99-1	APVC	APVA	
00-1	1,000	0,976	0,874	0,775
99-1	---	1,000	0,874	0,763
APVC	---	---	1,000	0,775
APVA	---	---	---	1,000

F 00-1	99-1	APVC	APVA	
00-1	1,000	0,938	0,810	0,677
99-1	---	1,000	0,803	0,674
APVC	---	---	1,000	0,719
APVA	---	---	---	1,000

M2-1	00-1	99-1	APVC	APVA
00-1	1,000	0,946	0,844	0,719
99-1	---	1,000	0,834	0,703
APVC	---	---	1,000	0,704
APVA	---	---	---	1,000

M2-2	00-1	99-1	APVC	APVA
00-1	1,000	0,901	0,563	0,246
99-1	---	1,000	0,577	0,232
APVC	---	---	1,000	0,191
APVA	---	---	---	1,000

SH	00-1	99-1	APVC	APVA
00-1	1,000	0,570	N.A.	0,178
99-1	---	1,000	N.A.	0,162
APVC	---	---	N.A.	N.A.
APVA	---	---	---	1,000

G 00-1	99-1	APVC	APVA	
00-1	1,000	0,326	N.A.	0,094
99-1	---	1,000	N.A.	0,107
APVC	---	---	N.A.	N.A.
APVA	---	---	---	1,000

5'L	00-1	99-1	APVC	APVA
00-1	1,000	0,921	N.A.	0,600
99-1	---	1,000	N.A.	0,594
APVC	---	---	N.A.	N.A.
APVA	---	---	---	1,000

Fig. 19

5'L: only the first 500 amino acid residues of 99-1 were available.
N.A.: sequence not available.

Fig.20

Amino acid sequence alignment of two prototype hMPV isolates

Nucleoprotein (N)

```
                10        20        30        40        50        60
            ....|....|....|....|....|....|....|....|....|....|....|
00-1    MSLQGIHLSDLSYKHAILKESQYTIKRDVGTTTAVTPSSLQQEITLLCGEILYAKHADYK 60
99-1    MSLQGIHLSDLSYKHAILKESQYTIKRDVGTTTAVTPSSLQQEITLLCGEILYTKHTDYK 60

                70        80        90       100       110       120
            ....|....|....|....|....|....|....|....|....|....|....|
00-1    YAAEIGIQYISTALGSERVQQILRNSGSEVQVVLTRTYSLGKIKNNKGEDLQMLDIHGVE 120
99-1    YAAEIGIQYICTALGSERVQQILRNSGSEVQVVLTKTYSLGKGKNSKGEELQMLDIHGVE 120

               130       140       150       160       170       180
            ....|....|....|....|....|....|....|....|....|....|....|
00-1    KSWVEEIDKEARKTMATLLKESSGNIPQNQRPSAPDTPIILLCVGALIFTKLASTIEVGL 180
99-1    KSWIEEIDKEARKTMVTLLKESSGNIPQNQRPSAPDTPIILLCVGALIFTKLASTIEVGL 180

               190       200       210       220       230       240
            ....|....|....|....|....|....|....|....|....|....|....|
00-1    ETTVRRANRVLSDALKRYPRMDIPKIARSFYDLFEQKVYHRSLFIEYGKALGSSSTGSKA 240
99-1    ETTVRRANRVLSDALKRYPRIDIPKIARSFYELFEQKVYYRSLFIEYGKALGSSSTGSKA 240

               250       260       270       280       290       300
            ....|....|....|....|....|....|....|....|....|....|....|
00-1    ESLFVNIFMQAYGAGQTMLRWGVIARSSNNIMLGHVSVQAELKQVTEVYDLVREMGPESG 300
99-1    ESLFVNIFMQAYGAGQTLLRWGVIARSSNNIMLGHVSVQSELKQVTEVYDLVREMGPESG 300

               310       320       330       340       350       360
            ....|....|....|....|....|....|....|....|....|....|....|
00-1    LLHLRQSPKAGLLSLANCPNFASVVLGNASGLGIIGMYRGRVPNTELFSAAESYAKSLKE 360
99-1    LLHLRQSPKAGLLSLANCPNFASVVLGNASGLGIIGMYRGRVPNTELFSAAESYARSLKE 360

               370       380       390
            ....|....|....|....|....|....
00-1    SNKINFSSLGLTDEEKEAAEHFLNVSDDSQNDYE 394
99-1    SNKINFSSLGLTDEEKEAAEHFLNMSGDNQDDYE 394
```

Fig.21

Phosphoprotein (P)

```
                10        20        30        40        50        60
        ....|....|....|....|....|....|....|....|....|....|....|....|
00-1    MSFPEGKDILFMGNEAAKLAEAFQKSLRKPGHKRSQSIIGEKVNTVSETLELPTISRPAK 60
99-1    MSFPEGKDILFMGNEAAKIAEAFQKSLKKSGHKRTQSIVGEKVNTISETLELPTISKPAR 60

                70        80        90        100       110       120
        ....|....|....|....|....|....|....|....|....|....|....|....|
00-1    PTIPSEPKLAWTDKGGATKTEIKQAIKVMDPIEEEESTEKKVLPSSDGKTPAEKKLKPST 120
99-1    SSTLLEPKLAWADNSGITKITEKPATKTTDPVEEEEFNEKKVLPSSDGKTPAEKKSKFST 120

                130       140       150       160       170       180
        ....|....|....|....|....|....|....|....|....|....|....|....|
00-1    NTKKKVSFTPNEPGKYTKLEKDALDLLSDNEEEDAESSILTFEERDTSSLSIEARLESIE 180
99-1    SVKKKVSFTSNEPGKYTKLEKDALDLLSDNEEEDAESSILTFEEKDTSSLSIEARLESIE 180

                190       200       210       220       230       240
        ....|....|....|....|....|....|....|....|....|....|....|....|
00-1    EKLSMILGLLRTLNIATAGPTAARDGIRDAMIGVREELIADIIKEAKGKAAEMMEEEMSQ 240
99-1    EKLSMILGLLRTLNIATAGPTAARDGIRDAMIGIREELIAEIIKEAKGKAAEMMEEEMNQ 240

                250       260       270       280       290
        ....|....|....|....|....|....|....|....|....|....|....
00-1    RSKIGNGSVKLTEKAKELNKIVEDESTSGESEEEEEPKDTQDNSQEDDIYQLIM 294
99-1    RSKIGNGSVKLTEKAKELNKIVEDESTSGESEEEEEPKETQDNNQGEDIYQLIM 294
```

Fig.22

Matrix protein (M)

```
                10        20        30        40        50        60
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1      MESYLVDTYQGIPYTAAVQVDLIEKDLLPASLTIWFPLFQANTPPAVLLDQLKTLTITTL 60
99-1      MESYLVDTYQGIPYTAAVQVDLVEKDLLPASLTIWFPLFQANTPPAVLLDQLKTLTITTL 60

                70        80        90       100       110       120
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1      YAASQNGPILKVNASAQGAAMSVLPKKFEVNATVALDEYSKLEFDKLTVCEVKTVYLTTM 120
99-1      YAASQNGPILKVNASAQGAAMSVLPKKFEVNATVALDEYSKLDFDKLTVCDVKTVYLTTM 120

               130       140       150       160       170       180
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1      KPYGMVSKFVSSAKSVGKKTHDLIALCDFMDLEKNTPVTIPAFIKSVSIKESESATVEAA 180
99-1      KPYGMVSKFVSSAKSVGKKTHDLIALCDFMDLEKNIPVTIPAFIKSVSIKESESATVEAA 180

               190       200       210       220       230       240
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1      ISSEADQALTQAKIAPYAGLIMIMTMNNPKGIFKKLGAGTQVIVELGAYVQAESISKICK 240
99-1      ISSEADQALTQAKIAPYAGLIMIMTMNNPKGIFKKLGAGTQVIVELGAYVQAESISRICK 240

               250
          ....|....|....
00-1      TWSHQGTRYVLKSR 254
99-1      SWSHQGTRYVLKSR 254
```

Fig.23

Fusion protein (F)

```
                10        20        30        40        50        60
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1      MSWKVVIIFSLLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEVGDVENLTC 60
99-1      MSWKVMIITSLLITPQHGLKESYLEESCSTITEGYLSVLRTGWYTNVFTLEVGDVENLTC 60

                70        80        90       100       110       120
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1      ADGPSLIKTELDLTKSALRELRTVSADQLAREEQIENPRQSRFVLGAIALGVATAAAVTA 120
99-1      TDGPSLIKTELDLTKSALRELKTVSADQLAREEQIENPRQSRFVLGAIALGVATAAAVTA 120

               130       140       150       160       170       180
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1      GVAIAKTIRLESEVTAIKNALKKTNEAVSTLGNGVRVLATAVRELKDFVSKNLTRAINKN 180
99-1      GIAIAKTIRLESEVNAIKGALKQTNEAVSTLGNGVRVLATAVRELKEFVSKNLTSAINRN 180

               190       200       210       220       230       240
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1      KCDIADLKMAVSFSQFNRRFLNVVRQFSDNAGITPAISLDLMTDAELARAVSNMPTSAGQ 240
99-1      KCDIADLKMAVSFSQFNRRFLNVVRQFSDNAGITPAISLDLMTDAELARAVSYMPTSAGQ 240

               250       260       270       280       290       300
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1      IKLMLENRAMVRRKGFGELIGVYGSSVIYMVQLPIFGVIDTPCWIVKAAPSCSGKKGNYA 300
99-1      IKLMLENRAMVRRKGFGILIGVYGSSVIYMVQLPIFGVIDTPCWIIKAAPSCSEKNGNYA 300

               310       320       330       340       350       360
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1      CLLREDQGWYCQNAGSTVYYPNEKDCETRGDHVFCDTAAGINVAEQSKECNINISTTNYP 360
99-1      CLLREDQGWYCKNAGSTVYYPNEKDCETRGDHVFCDTAAGINVAEQSRECNINISTTNYP 360

               370       380       390       400       410       420
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1      CKVSTGRHPISMVALSPLGALVACYKGVSCSIGSNRVGIIKQLNKGCSYITNQDADTVTI 420
99-1      CKVSTGRHPISMVALSPLGALVACYKGVSCSIGSNWVGIIKQLPKGCSYITNQDADTVTI 420

               430       440       450       460       470       480
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1      DNTVYQLSKVEGEQHVIKGRPVSSSFDPVKFPEDQFNVALDQVFESIENSQALVDQSNRI 480
99-1      DNTVYQLSKVEGEQHVIKGRPVSSSFDPIKFPEDQFNVALDQVFESIENSQALVDQSNKI 480

               490       500       510       520       530
          ....|....|....|....|....|....|....|....|....|....|....
00-1      LSSAEKGNTGFIIVIILIAVLGSTMILVSVFIIIKKTKKPTGAPPELSGVTNNGFIPHN 539
99-1      LNSAEKGNTGFIIVVILVAVLGLTMISVSIIIIIKKTRKPTGAPPELNGVTNCGFIPHS 539
```

Fig.24

22K protein (M2-1)

```
                10        20        30        40        50        60
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1      MSRKAPCKYEVRGKCNRGSECKFNHNYWSWPDRYLLIRSNYLLNQLLRNTDRADGLSIIS 60
99-1      MSRKAPCKYEVRGKCNRGSDCKFNHNYWSWPDRYLLLRSNYLLNQLLRNTDKADGLSIIS 60

                70        80        90       100       110       120
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1      GAGREDRTQDFVLGSTNVVQGYIDDNQSITKAAACYSLHNIIKQLQEVEVRQARDNKLSD 120
99-1      GAGREDRTQDFVLGSTNVVQGYIDDNQGITKAAACYSLHNIIKQLQETEVRQARDNKLSD 120

               130       140       150       160       170       180
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1      SKHVALHNLVLSYMEMSKTPASLINNLKRLPREKLKKLAKLIIDLSAGAENDSSYALQDS 180
99-1      SKHVALHNLILSYMEMSKTPASLINNLKKLPREKLKKLARLIIDLSAGTDNDSSYALQDS 180


          ....|..
00-1      ESTNQVQ 187
99-1      ESTNQVQ 187
```

Fig.25

M2-2 protein (M2-2)

```
                10        20        30        40        50        60
      ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  MTLHMPCKTVKALIKCSEHGPVFITIEVDDMIWTHKDLKEALSDGIVKSHTNIYNCYLEN 60
99-1  MTLHMPCKTVKALIKCSKHGPKFITIEADDMIWTHKELKETLSDGIVKSHTNIYSCYLEN 60

                70
      ....|....|.
00-1  IEIIYVKAYLS 71
99-1  IEIIYVKTYLS 71
```

Fig.26

Short hydrophobic protein (SH)

```
                10        20        30        40        50        60
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1   MITLDVIKSDGSSKTCTHLKKIIKDHSGKVLIVLKLILALLTFLTVTITINYIKVENNLQ 60
99-1   MKTLDVIKSDGSSETCNQLKKIIKKHSGKVLIALKLILALLTFFTATITVNYIKVENNLQ 60

                70        80        90       100       110       120
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1   ICQSKTESDKKDSSSNTTSVTTKTTLNHDITQYFKSLIQRYTNSAIN-SDTCWKINRNQC 119
99-1   ACQPKNESDKKVTKPNTTSTTIRPTPDPTVVHHLKRLIQRHTNSVTKDSDTCWRIHKNQR 120

               130       140       150       160       170       180
          ....|....|....|....|....|....|....|....|....|....|....|....|
00-1   TNITTYKFLCFKSEDTKTNNCDKLTDLCRNKPKPAVGVYHIVECHCIYTVKWKCYHYPTD 179
99-1   TNIKIYKFLCSGFTNSKGTDCEEPTALCDKKLKTIVEKHRKAECHCLHTTEWGCLHP--- 177

          ....
00-1   ETQS 183
99-1   ---- 177
```

Fig.27

Attachment glycoprotein (G)

```
                10        20        30        40        50        60
      ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  MEVKVENIRTIDMLKARVKNRVARSKCFKNASLVLIGITTLSIALNIYLIINYKMQKNTS 60
99-1  MEVRVENIRAIDMFKAKIKNRIRSSRCYRNATLILIGLTALSMALNIFLIIDHATLRNMI 60

                70        80        90        100       110       120
      ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  ESEHHTSSSPMESSRETPTVPTDNSDTNSSPQHPTQQSTEGSTLYFAASASSSPETEPTST 120
99-1  KTENCANMPSAEPSKKTPMTSTAGPNTKPNPQQATQWTTENSTSPVATPEGHPYTGTTQT 120

                130       140       150       160       170       180
      ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  PDTTNRPPFVDTHTTPPSASRTKTSPAVHTKNNPRTSSRTHSPPRATTRTARRTTTLRTS 180
99-1  SDTTAPQQTTDKHTAPLKSTNEQITQTTTEKKTIRATTQKREKGKENTNQTTSTAATQTT 180

                190       200       210       220       230
      ....|....|....|....|....|....|....|....|....|....|....|.
00-1  STRKRPSTASVQPDISATTHKNEEASPASPQTSASTTRIQRKSVEANTSTTYNQTS 236
99-1  NTTNQIRNASET-----ITTSDRPRTDTTTQSSEQTTRATDPSSPPHHA------- 224
```

Fig.28

N-terminus of polymerase protein (L)

```
                10        20        30        40        50        60
           ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  MDPLNESTVNVYLPDSYLKGVISFSETNAIGSCLLKRPYLKNDNTAKVAIENPVIEHVRL 60
99-1  MDPFCESTVNVYLPDSYLKGVISFSETNAIGSCLLKRPYLKNDNTAKVAVENPVVEHVRL 60

                70        80        90       100       110       120
           ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  KNAVNSKMKISDYKIVEPVNMQHEIMKNVHSCELTLLKQFLTRSKNISTLKLNMICDWLQ 120
99-1  RNAVMTKMKISDYKVVEPVNMQHEIMKNIHSCELTLLKQFLTRSKNISSLKLNMICDWLQ 120

               130       140       150       160       170       180
           ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  LKSTSDDTSILSFIDVEFIPSWVSNWFSNWYNLNKLILEFRKEEVIRTGSILCRSLGKLV 180
99-1  LKSTSDNTSILNFIDVEFIPVWVSNWFSNWYNLNKLILEFRREEVIRTGSILCRSLGKLV 180

               190       200       210       220       230       240
           ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  FVVSSYGCIVKSNKSKRVSFFTYNQLLTWKDVMLSRFNANFCIWVSNSLNENQEGLGLRS 240
99-1  FIVSSYGCVVKSNKSKRVSFFTYNQLLTWKDVMLSRFNANFCIWVSNNLNKNQEGLGLRS 240

               250       260       270       280       290       300
           ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  NLQGILTNKLYETVDYMLSLCCNEGFSLVKEFEGFIMSEILRITEHAQFSTRFRNTLLNG 300
99-1  NLQGMLTNKLYETVDYMLSLCCNEGFSLVKEFEGFIMSEILKITEHAQFSTRFRNTLLNG 300

               310       320       330       340       350       360
           ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  LTDQLTKLKNKNRLRVHGTVLENNDYPMYEVVLKLLGDTLRCIKLLINKNLENAAELYYI 360
99-1  LTEQLSVLKAKNRSRVLGTILENNNYPMYEVVLKLLGDTLKSIKLLINKNLENAAELYYI 360

               370       380       390       400       410       420
           ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  FRIFGHPMVDERDAMDAVKLNNEITKILRTESLTELRGAFILRIIKGFVDNNKRWPKIKN 420
99-1  FRIFGHPMVDEREAMDAVKLNNEITKILKLESLTELRGAFILRIIKGFVDNNKRWPKIKN 420

               430       440       450       460       470       480
           ....|....|....|....|....|....|....|....|....|....|....|....|
00-1  LKVLSKRWTMYFKAKSYPSQLELSEQDFLELAAIQFEQEFSVPEKTNLEMVLNDKAISPP 480
99-1  LKVLSKRWAMYFKAKSYPSQLELSVQDFLELAAVQFEQEFSVPEKTNLEMVLNDKAISPP 480

               490
           ....|....|....|....
00-1  KRLIWSVYPKNYLPEKIKN 499
99-1  KKLIWSVYPKNYLPETIKN 499
```

Fig. 29

+ = positive; - = negative; T = throatswabs; NO = nose swab; N = not done; ? = not sure; D = dead; 0 to 12: days post infection. 2e infection is only tested on nose swabs.

nr	1e infection	swab	0	1	2	3	4	5	8	10	11	12	2e infection	0	1	2	3	4	5
1	00-1	T	-	+	+	+	-	+	+	+	-	-	99-1	N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	+	-	-		-	-	-	-	-	-
2	00-1	T	-	+	+	+	+	+	-	-	-	D		N	N	N	N	N	N
		NO		+	+	+	+	+	N	+	-	D		-	-	-	-	-	-
3	00-1	T	-	-	?	-	-	-	-	-	-	N	99-1	N	N	?	N	N	N
		NO		+	?	?		-	N	-	-	-		-	-	?	+	+	-
4	00-1	T	-	+	+	+	+	+	-	?	-	N	00-1	N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	?	-	-		-	-	-	+	-	-
5	00-1	T	-	?	+	+	+	+	+	+	-	N	00-1	N	N	N	N	N	N
		NO		+	+	+	+	+	N	+	-	-		-	-	-	-	-	-
6	00-1	T	-	-	+	+	+	+	-	+	-	N	00-1	N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	+	+	?		-	-	-	-	-	-
7	99-1	T	-	-	-	+	+	-	+	D	-	-		N	N	N	N	N	N
		NO	-	-	--	+	+	+	N	D	-	-		-	-	-	-	-	-
8	99-1	T	-	-	+	+	-	-	-	-	-	N	00-1	N	N	N	N	N	N
		NO	--	?	-	+	+	?	N	-	-	--		-	-	+	+	+	+
9	99-1	T	-	-	-	-	-	-	-	-	-	N	00-1	N	N	N	N	N	N
		NO	-	-	-	-	+	+	N	-	-	--		-	?	+	+	-	-
10	99-1	T	-	-	-	+	+	-	-	-	-	N	99-1	N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	-	-	--		-	-	-	-	-	-
11	99-1	T	-	-	+	+	+	-	-	-	-	N	99-1	N	N	N	N	N	N
		NO	-	+	?	+	+	+	N	-	-	-		-	-	-	+	-	-
12	99-1	T	-	-	+	+	?	-	-	-	-	N	99-1	N	N	N	N	N	N
		NO	-	+	+	+	+	+	N	-	-	-		-	-	-	-	-	-

Fig. 30A

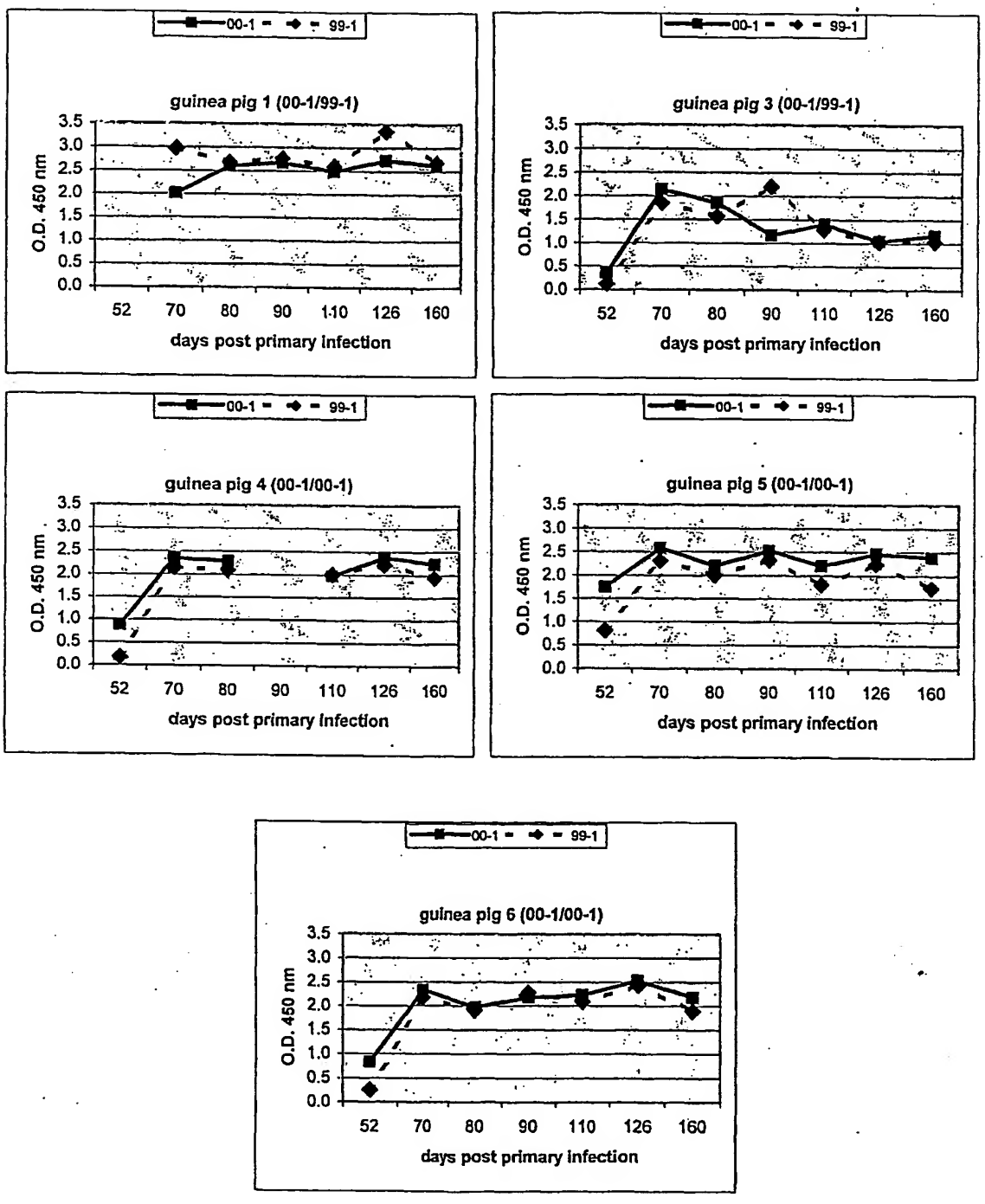

00-1
99-1
guinea pig 1 (00-1/99-1)
guinea pig 3 (00-1/99-1)
guinea pig 4 (00-1/00-1)
guinea pig 5 (00-1/00-1)
guinea pig 6 (00-1/00-1)
O.D. 450 nm
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
52
70
80
90
110
126
160
days post primary infection

Fig. 30B

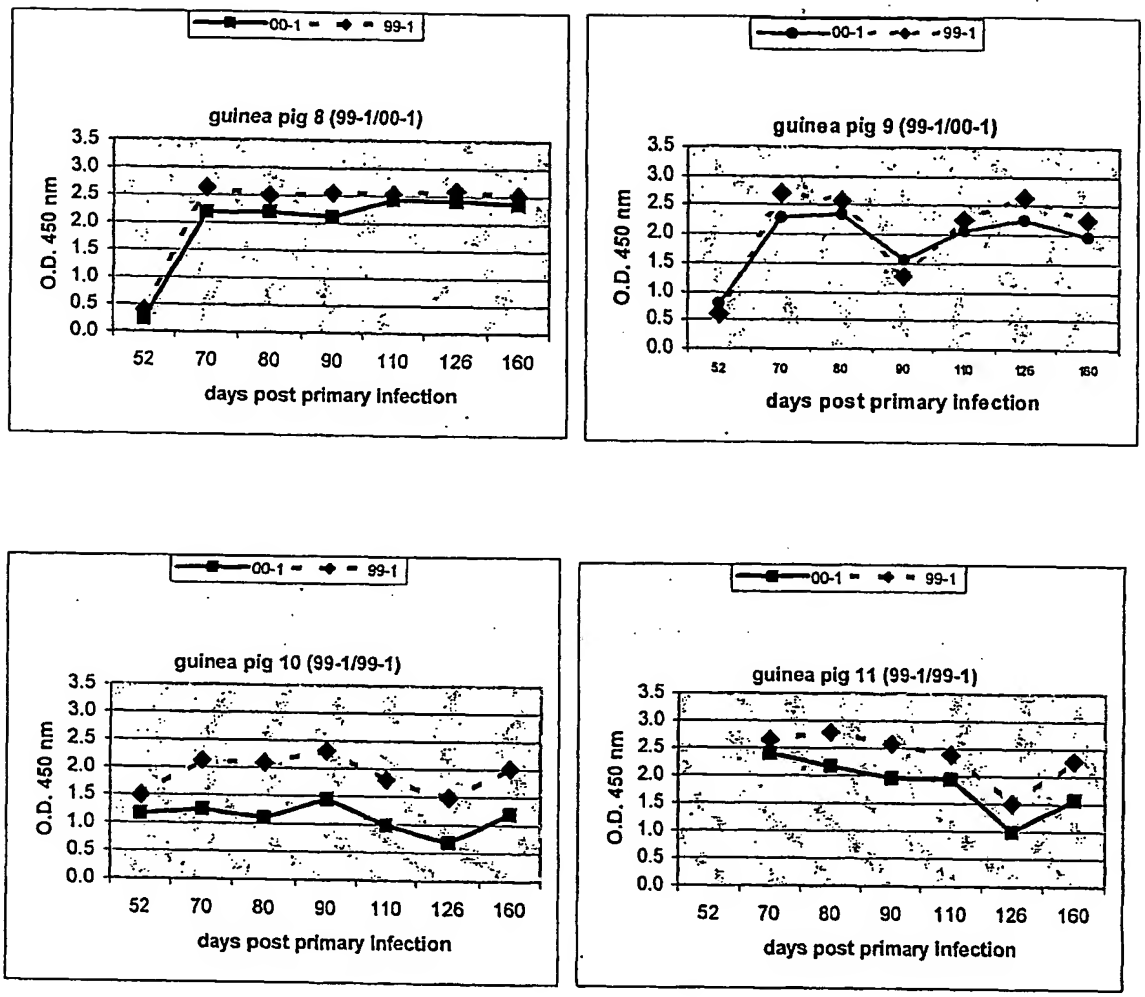

00-1
99-1
guinea pig 8 (99-1/00-1)
guinea pig 9 (99-1/00-1)
guinea pig 10 (99-1/99-1)
guinea pig 11 (99-1/99-1)
O.D. 450 nm
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.5
52
70
80
90
110
126
160
days post primary infection

Fig. 31

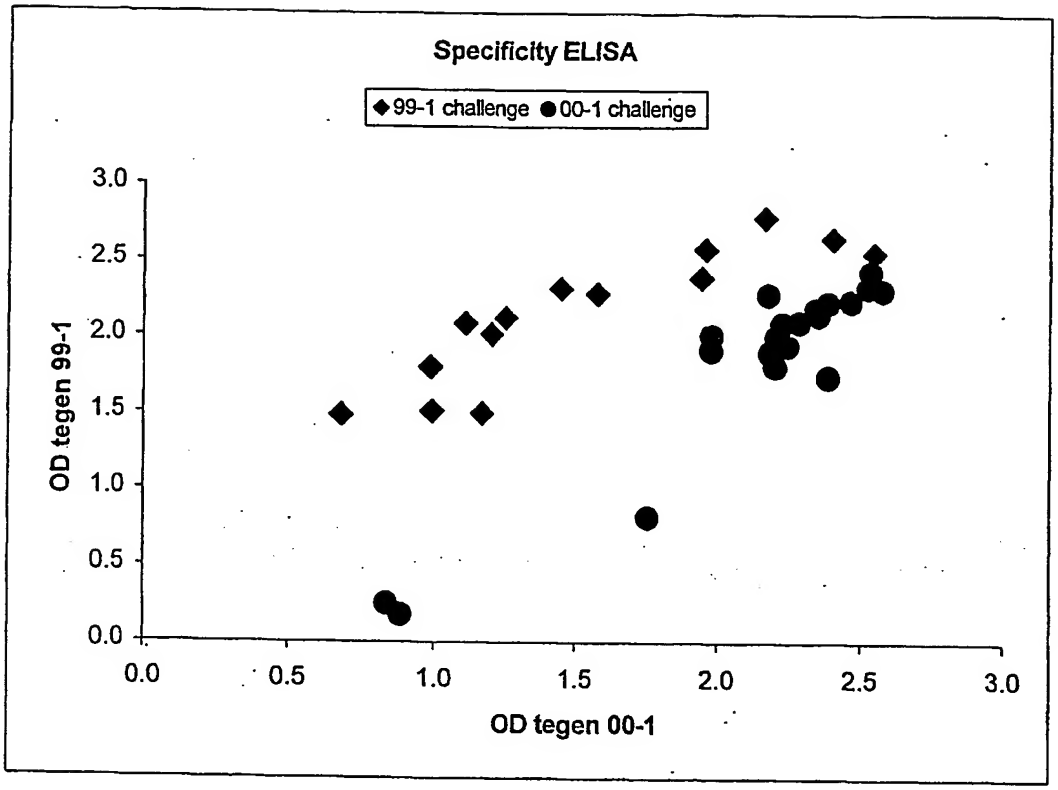

Specificity ELISA
◆99-1 challenge ●00-1 challenge
OD tegen 99-1
OD tegen 00-1
3.0
2.5
2.0
1.5
1.0
0.5
0.0
0.0
0.5
1.0
1.5
2.0
2.5
3.0

Fig. 32

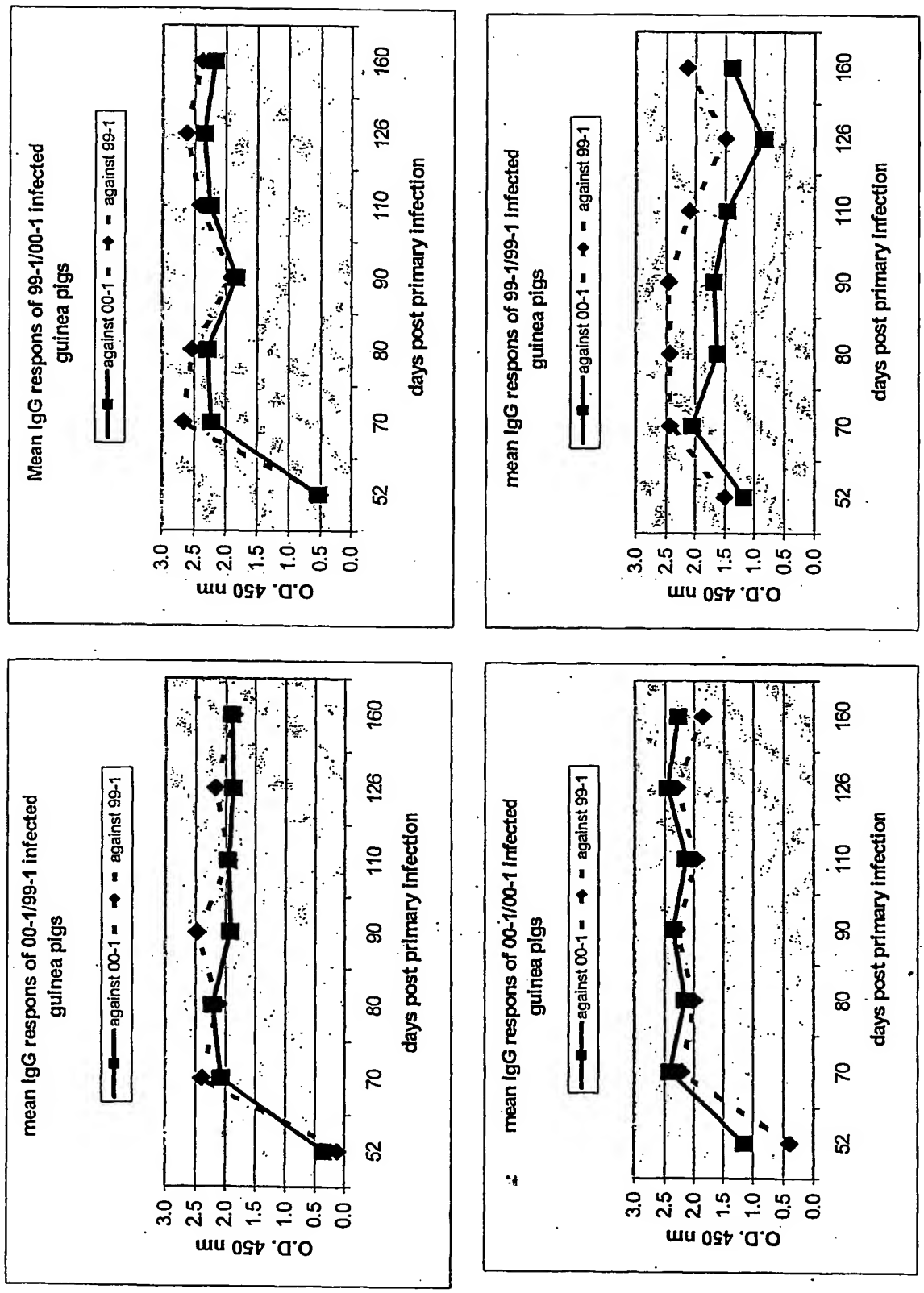

Mean IgG respons of 99-1/00-1 infected guinea pigs
against 00-1
against 99-1
O.D. 450 nm
days post primary infection
mean IgG respons of 99-1/99-1 infected guinea pigs
mean IgG respons of 00-1/99-1 infected guinea pigs
mean IgG respons of 00-1/00-1 infected guinea pigs

Fig. 33

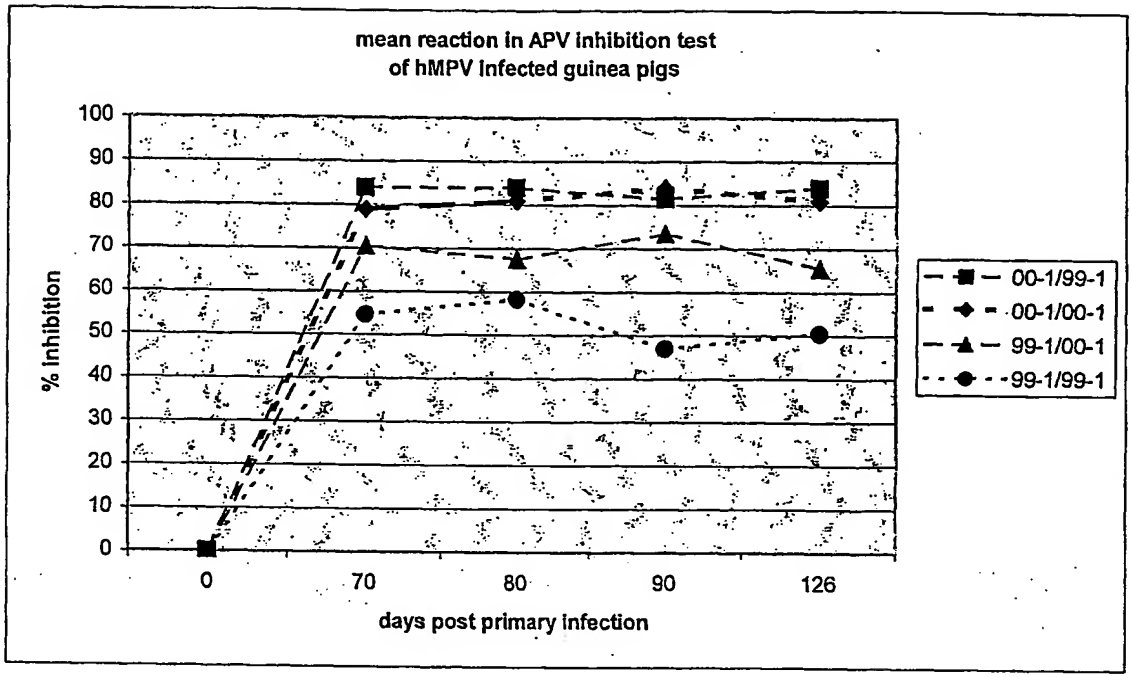

mean reaction in APV inhibition test
of hMPV infected guinea pigs
% inhibition
100
90
80
70
60
50
40
30
20
10
0
0
70
80
90
126
days post primary infection
00-1/99-1
00-1/00-1
99-1/00-1
99-1/99-1

Fig. 34

	Against 00-1	Against 99-1	Against APV-C
1 infection with 00-1			
2 infections with 00-1			
1infection with 99-1			
2 infections with 00-1			

Fig. 35

+ = positive; - = negative; N = not done; ? = not sure; 0 to 10: days post infection

nr	1st infection	0	2	3	4	5	6	7	8	9	11	2nd infection	0	1	2	3	4	5	7	10
3	00-1	-	-	-	+	+	+	+	+	N	-		-	+	+	+	+	-	?	-
6	00-1	-	+	+	+	+	+	+	-	-	-		-	+	+	+	+	+	-	-

Fig. 36A

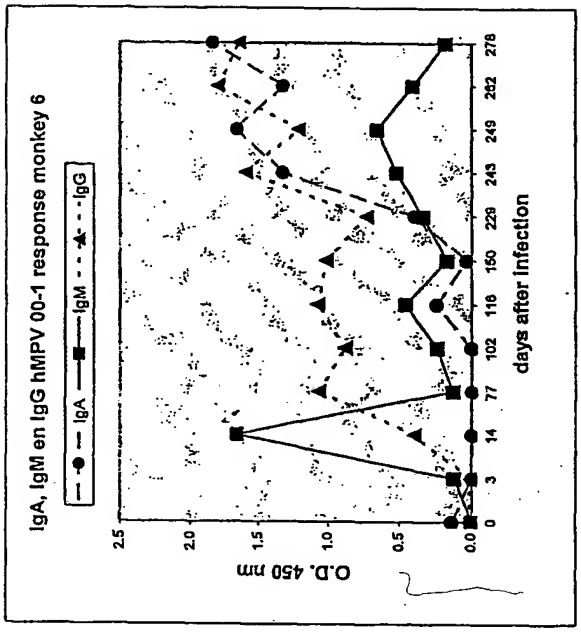


Fig. 36B

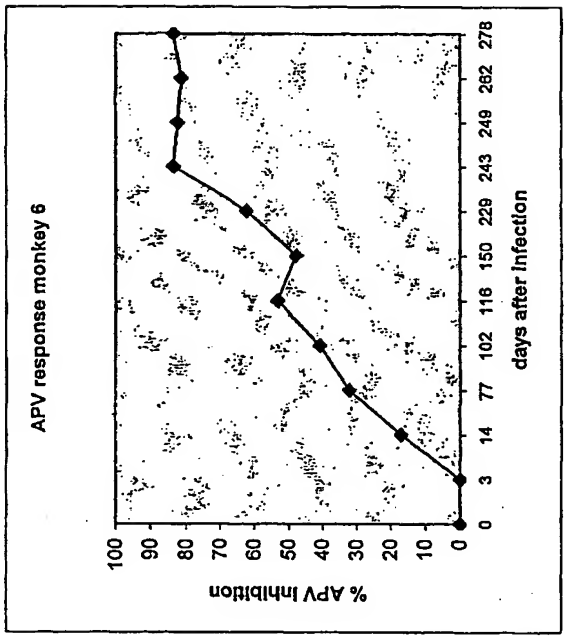
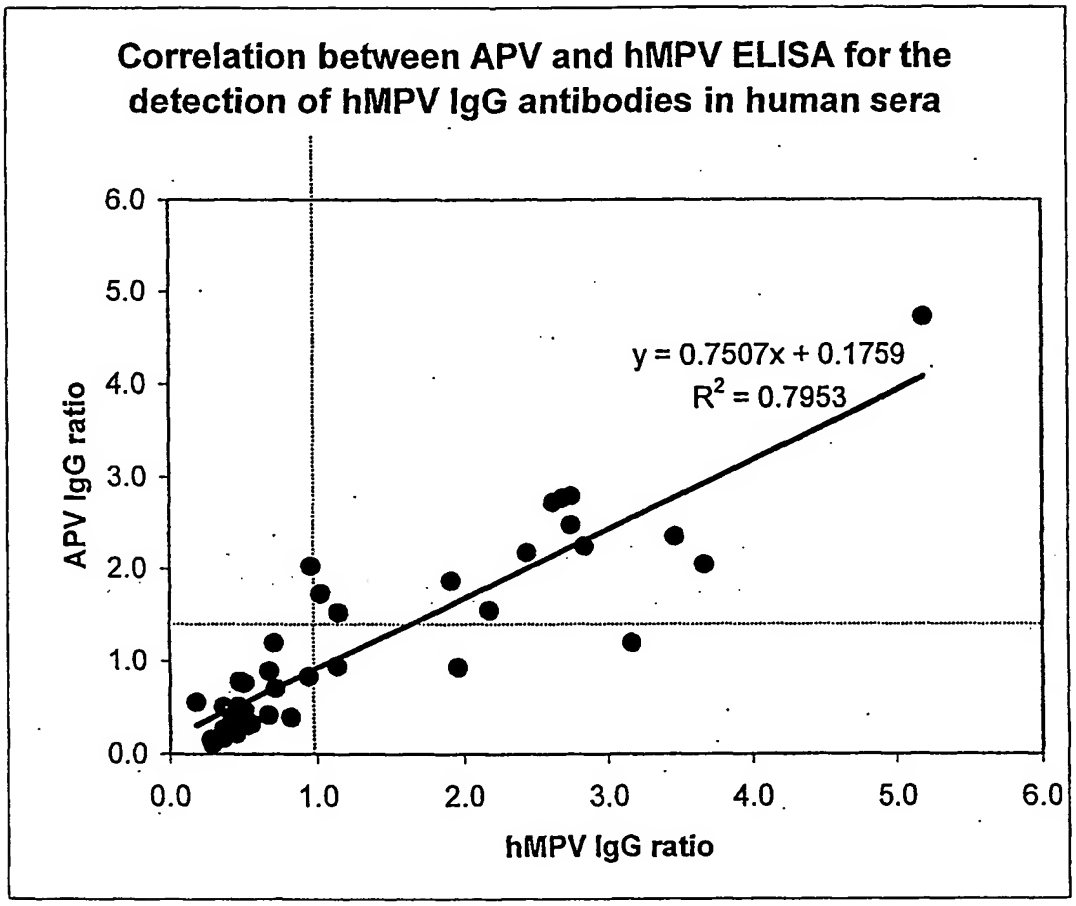


Fig. 37


Correlation between APV and hMPV ELISA for the detection of hMPV IgG antibodies in human sera
y = 0.7507x + 0.1759
R2 = 0.7953
APV IgG ratio
hMPV IgG ratio
0.0
1.0
2.0
3.0
4.0
5.0
6.0